

Gencore version 5.1.6
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 protein - protein search, using sw model
 on: September 20, 2004, 17:27:20 ; Search time 52 Seconds
 (without alignments)
 43.469 Million cell updates/sec
 File: AUDET-SQ01
 Effect score: 46
 Sequence: 1 gsfifbelw 8
 Scoring table: BLOSUM62
 Gapext: 0.5
 Searched: 1586107 seqs, 282547505 residues
 Abi 005: raw/hdm a
 26 2/ 58.7 12 3 ABB73170 Mdm/hdm a
 27 2/ 58.7 12 3 ABB73183 Mdm/hdm a
 28 2/ 58.7 12 3 ABB73171 Mdm/hdm a
 29 2/ 58.7 12 3 ABB73182 Mdm/hdm a
 30 2/ 58.7 12 3 AAY57799 TRAM-inte
 31 2/ 58.7 13 3 AAY57799 Biotinyl1a
 32 2/ 58.7 14 5 Abi05528 Immunodom
 33 2/ 58.7 15 2 AAR54909 Immunodom
 34 2/ 58.7 15 2 AAR54910 Immunodom
 35 2/ 58.7 15 2 AAR89914 p53 prote
 36 2/ 58.7 15 2 AAY06310 Human p53
 37 2/ 58.7 15 3 AAY99001 HLA class
 38 2/ 58.7 15 3 AB22780 Human amy
 39 2/ 58.7 15 3 AAB29161 Peptide #
 40 2/ 58.7 15 3 AAB29159 Peptide #
 41 2/ 58.7 15 3 AAB29167 Peptide #
 42 2/ 58.7 15 3 AAB29160 Peptide #
 43 2/ 58.7 15 3 AAB29157 Peptide #
 44 2/ 58.7 15 4 AAG89730 p53 DR3
 45 2/ 58.7 15 4 AAG89500 p53 DR 3a

ATTACHMENTS

卷之三

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

-abase : A_Geneseq_28Jan04;*

1: _geneseqp1980s;*

2: geneseqp1990s;*

3: geneseqp2000s;*

4: geneseqp2001s;*

5: geneseqp2002s;*

6: geneseqp2003ab;*

7: geneseqp2003bs;*

RESULT 1
 AAB86005
 ID AAB86005 standard; peptide; 12 AA.
 XX
 AC AAB86005;
 XX
 DT 12-JUL-2001 (first entry)
 XX
 DE DCM-associated peptide #5.
 XX
 KW DCM; dilatative cardiomyopathy; autoantibody; cardiant;
 KW beta-1 adrenergic activated antibody; immunosuppressive.

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

סעיפים

Result	No.	Score	Query Match	Length	DB	ID	Description	PF	XX
1	46	100.0	12	4	AAB86005	Aab86005 DCM-assoc	21-SEP-2000; 2000WO-EP009241.	PR	XX
2	46	100.0	13	4	AAB86006	Aab86006 DCM-assoc	21-SEP-1999; 99EP-00118630.	PR	XX
3	46	100.0	14	4	AAB86012	Aab86012 DCM-assoc	21-SEP-1999; 99EP-00118631.	PA	XX
4	46	100.0	14	4	AAB86020	Aab86020 DCM- autoa	'AFFI-) AFFINA IMMUNTECHNIK GMBH.	PI	XX
5	46	100.0	14	4	AAB86013	Aab86013 DCM-assoc		XX	XX
6	46	100.0	15	4	AAB86021	Aab86021 DCM- autoa	Roemspeck W, Kunze R, Wallukat G, Dierenfeld M;	DR	XX
7	30	65.2	13	4	AAB86009	Aab86009 DCM-assoc	New peptide useful for combating the autoantibodies that are responsible for dilatative cardiomyopathy.	PT	XX
8	30	67.2	13	4	AAB86007	Aab86007 DCM-assoc	Claim 3; Page 20; 29pp; German.	PT	XX
9	30	65.2	13	5	AAM47221	Aam47221 Dilated C	Claim 3; Page 20; 29pp; German.	PS	XX
10	30	65.2	15	4	AAB86028	Aab86028 DCM- autoa		CC	XX
11	30	65.2	15	4	AAB86017	Aab86017 DCM-assoc	This invention describes a novel peptide (P1) which can be used for (1)	CC	XX
12	30	65.2	15	4	AAB86014	Aab86014 DCM-assoc	isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid	CC	XX
13	30	65.2	15	4	AAB86022	Aab86022 DCM- autoa	phase; and (2) a chromatographic apparatus with (P1) bound. The products	CC	XX
14	30	65.2	15	4	AAO20307	Aao20307 Human pie	of the invention have cardiotonic and immunosuppressive activity.	CC	XX
15	29	63.0	15	6	ABJ37231	Rhodopsin	(P1) is used to produce medicine to combat beta-1 adrenergic activated	CC	XX
16	27	58.7	11	2	AAM1231	Peptide A	autoantibodies having a causal pathological relationship with dilatative	CC	XX
17	27	58.7	11	4	AAU27152	Human Leu	cardiomyopathy. This sequence represents specifically claimed peptide	CC	XX
18	27	58.7	11	4	AAU26842	Aau26842 Human Leu	used to illustrate the method of the invention	CC	XX
19	27	58.7	11	5	AAM52269	Aam52269 Miniature		CC	XX
20	27	58.7	12	2	AAM37181	Aam37181 Human p53	Sequence 12 AA;	CC	XX
21	27	58.7	12	2	AAM37188	Aam37188 Human onc	SQ	XX	XX
22	27	58.7	12	2	AAM37189	Aam37189 Human onc		CC	XX
23	27	58.7	12	3	AAB17076	Aab17076 Mdm/hdm a		CC	XX
24	27	58.7	12	3	AAB17087	Aab17087 Mdm/hdm a		CC	XX
25	27	58.7	12	3	AAB17088	Aab17088 Mdm/hdm a		CC	XX
26	27	58.7	12	3	AAB17089	Aab17089 Mdm/hdm a		CC	XX
27	58.7	12	3	AAB17090	Aab17090 Mdm/hdm a		CC	XX	

Sequence 12 AA:	Query Match Exact 100% similarity	Score 46;	DB 4;	Length 12;
SQ	XX	100.0%	None	None

PF 21-SEP-1999; 99DE-01045211.
 XX PR 21-SEP-1999; 99DE-01045211.
 XX (AFFI-) AFFINA IMMUNTECHNIK GMBH.
 XX PA Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
 XX PI DR WPI: 2001-301259/32.
 XX PT New autoantibody-binding peptides with an amino acid sequence
 PT corresponding a beta-1-adrenergic receptor group useful for treating
 PT dilatative cardiomyopathy.
 XX SQ Sequence 5; 8pp; German.

This invention describes novel peptides (I) with an amino acid sequence corresponding a beta-1-adrenergic receptor group recognized by autoantibodies associated with dilatative cardiomyopathy (DCM). The invention also describes a chromatographic device comprising (I) bound to a solid phase. The products of the invention have cardiotropic activity. (I) are useful for treating DCM by binding autoantibodies directed against myocardial beta-1-adrenergic receptor, either by neutralizing the antibodies *in vivo* or by extracorporeal treatment of blood or plasma with (I) immobilized on a solid phase. This sequence represents a specifically claimed peptide used to illustrate the method of the invention

PS Sequence 14 AA;

XX This invention describes a novel peptide (P1), which can be used for (1) isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid phase; and (2) a chromatographic apparatus with (P1) bound. The products of the invention have cardiotropic and immunosuppressive activity. (P1) is used to produce medicine to combat beta-1 adrenergic activated autoantibodies having a causal pathological relationship with dilatative cardiomyopathy. This sequence represents a specifically claimed peptide used to illustrate the method of the invention

XX SQ Sequence 15 AA;

Query Match 100 %; Score 46; DB 4; Length 15;
 Best Local Similarity 100 %; Pred. No. 0.08;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSFFSELW 8
 Db 3 GSFFSELW 10

RESULT 6
 ID AAB86021 standard; peptide; 15 AA.
 XX ID AAB86021 standard; peptide; 15 AA.
 XX AC AAB86021;
 XX DT 12-JUL-2001 (first entry)
 XX DE DCM autoantibody-associated peptide #2.
 XX KW DCM; dilatative cardiomyopathy; beta-1-adrenergic receptor; cardiotropic; autoantibody; myocardial.
 XX OS Synthetic.
 XX Key Location/Qualifiers
 XX FT Modified-site 1 /note= "N-terminal acetylated"
 XX FT Modified-site 15 /note= "C-terminal amide"
 XX FT DE1945211-A1.
 XX PN PR 21-SEP-1999; 99DE-01045211.
 XX PD 29-MAR-2001.
 XX PF 21-SEP-1999; 99DE-01045211.
 XX PR 21-SEP-1999; 99DE-01045211.
 XX PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.
 XX PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
 XX DR WPI; 2001-301259/32.
 XX PT New autoantibody-binding peptides with an amino acid sequence
 PT corresponding a beta-1-adrenergic receptor group useful for treating
 PT dilatative cardiomyopathy.
 XX PS Claim 2; Page 5; 8pp; German.

This invention describes novel peptides (I) with an amino acid sequence corresponding a beta-1-adrenergic receptor group recognized by autoantibodies associated with a chromatographic device comprising (I) bound to a solid phase. The products of the invention have cardiotropic activity. (I) are useful for treating DCM by binding autoantibodies directed against myocardial beta-1-adrenergic receptors, either by neutralizing the antibodies *in vivo* or by extracorporeal treatment of blood or plasma with

PR 21-SEP-1999; 99EP-00118630.
 XX PR 21-SEP-1999; 99EP-00118631.
 XX PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.
 XX PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
 XX DR WPI; 2001-335469/35.
 XX PT New peptide useful for combating the autoantibodies that are responsible

CC (1) immobilized on a solid phase. This sequence represents a specifically
CC claimed peptide used to illustrate the method of the invention
XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 46; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OS Synthetic.
KW beta-1 adrenergic activated antibody; immuno suppressive.

QY 1 GSFFSEWLW 8

Db 3 GSFFSEWLW 10

RESULT 7

AAB86009 standard; peptide; 13 AA.

ID AAB86009

AC AAB86009;

XX

DT 12-JUL-2001 (first entry)

DE DCM-associated peptide #7.

XX

PR 21-SEP-1999;

XX

99EP-00118630.

PR 21-SEP-1999;

XX

99EP-00118631.

PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.

XX

PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;

XX

DR WPI; 2001-335469/35.

XX

New peptide useful for combating the autoantibodies that are responsible

PT for dilatative cardiomyopathy.

XX

PS Claim 3; Page 21; 29pp; German.

XX

This invention describes a novel peptide (P1) which can be used for (1)

CC isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid

CC phase; and (2) a chromatographic apparatus with (P1) bound. The products

CC of the invention have cardiotonic and immunosuppressive activity. (P1) is

CC used to produce medicine to combat beta-1 adrenergic activated

CC autoantibodies having a causal pathological relationship with dilatative

CC cardiomyopathy. This sequence represents a specifically claimed peptide

CC used to illustrate the method of the invention

XX

Sequence 13 AA;

XX

Query Match 65.2%; Score 30; DB 4; Length 13;

Best Local Similarity 50.0%; Pred. No. 70;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OS Synthetic.

KW betal adreno receptor;

XX

DB WO200121660-A1.

XX

PD 29-MAR-2001.

XX

PR 21-SEP-2000; 2000WO-EP009241.

XX

99EP-00118630.

PR 21-SEP-1999;

XX

99EP-00118631.

PR 21-SEP-1999;

XX

PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.

XX

PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;

XX

DR WPI; 2001-335469/35.

XX

New peptide useful for combating the autoantibodies that are responsible

PT for dilatative cardiomyopathy.

XX

PS Claim 3; Page 21; 29pp; German.

XX

This invention describes a novel peptide (P1) which can be used for (1)

CC isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid

CC phase; and (2) a chromatographic apparatus with (P1) bound. The products

CC of the invention have cardiotonic and immunosuppressive activity. (P1) is

CC used to produce medicine to combat beta-1 adrenergic activated

CC autoantibodies having a causal pathological relationship with dilatative

CC cardiomyopathy. This sequence represents a specifically claimed peptide

CC used to illustrate the method of the invention

XX

Sequence 13 AA;

XX

Query Match 65.2%; Score 30; DB 4; Length 13;

Best Local Similarity 50.0%; Pred. No. 70;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OS Synthetic.

KW betal adreno receptor;

XX

DB WO2001176662-A1.

XX

PD 18-OCT-2001.

XX

PR 09-APR-2001; 2001WO-JP003026.

XX

07-APR-2000; 2000JP-00106915.

CC (1) immobilized on a solid phase. This sequence represents a specifically
CC claimed peptide used to illustrate the method of the invention
XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 46; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OS Synthetic.
KW beta-1 adrenergic activated antibody; immuno suppressive.

QY 1 GSFFSEWLW 8

Db 3 GTLFSSDFW 10

RESULT 8

AAB86007

ID AAB86007

AC AAB86007;

XX

DT 12-JUL-2001 (first entry)

DE DCM-associated peptide #7.

XX

PR 21-SEP-1999;

XX

99EP-00118630.

PR 21-SEP-1999;

XX

99EP-00118631.

PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.

XX

PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;

XX

DR WPI; 2001-335469/35.

XX

New peptide useful for combating the autoantibodies that are responsible

PT for dilatative cardiomyopathy.

XX

PS Claim 3; Page 21; 29pp; German.

XX

This invention describes a novel peptide (P1) which can be used for (1)

CC isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid

CC phase; and (2) a chromatographic apparatus with (P1) bound. The products

CC of the invention have cardiotonic and immunosuppressive activity. (P1) is

CC used to produce medicine to combat beta-1 adrenergic activated

CC autoantibodies having a causal pathological relationship with dilatative

CC cardiomyopathy. This sequence represents a specifically claimed peptide

CC used to illustrate the method of the invention

XX

Sequence 13 AA;

XX

Query Match 65.2%; Score 30; DB 4; Length 13;

Best Local Similarity 50.0%; Pred. No. 70;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OS Synthetic.

KW betal adreno receptor;

XX

DB WO200121660-A1.

XX

PD 29-MAR-2001.

XX

PR 21-SEP-2000; 2000WO-EP009241.

XX

99EP-00118630.

PR 21-SEP-1999;

XX

99EP-00118631.

PR 21-SEP-1999;

XX

PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.

XX

PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;

XX

DR WPI; 2001-335469/35.

XX

New peptide useful for combating the autoantibodies that are responsible

PT for dilatative cardiomyopathy.

XX

PS Claim 3; Page 21; 29pp; German.

XX

This invention describes a novel peptide (P1) which can be used for (1)

CC isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid

CC phase; and (2) a chromatographic apparatus with (P1) bound. The products

CC of the invention have cardiotonic and immunosuppressive activity. (P1) is

CC used to produce medicine to combat beta-1 adrenergic activated

CC autoantibodies having a causal pathological relationship with dilatative

CC cardiomyopathy. This sequence represents a specifically claimed peptide

CC used to illustrate the method of the invention

XX

Sequence 13 AA;

XX

Query Match 65.2%; Score 30; DB 4; Length 13;

Best Local Similarity 50.0%; Pred. No. 70;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OS Synthetic.

KW betal adreno receptor;

XX

DB WO2001176662-A1.

XX

PD 18-OCT-2001.

XX

PR 09-APR-2001; 2001WO-JP003026.

XX

07-APR-2000; 2000JP-00106915.

CC (1) immobilized on a solid phase. This sequence represents a specifically
CC claimed peptide used to illustrate the method of the invention
XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 46; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OS Synthetic.
KW beta-1 adrenergic activated antibody; immuno suppressive.

QY 1 GSFFSEWLW 8

Db 3 GTLFSSDFW 10

RESULT 9

AAM47221

ID AAM47221

AC AAM47221;

XX

Dilated cardiomyopathy absorbents related peptide #1.

XX

DE Dilated cardiomyopathy absorbents related peptide #1.

XX

KW Dilated cardiomyopathy absorbent;

XX

M2 muscarine receptor; antibody.

XX

AC AAM47221;

XX

12-FEB-2002 (first entry)

XX

Query Match 65.2%; Score 30; DB 4; Length 13;

Best Local Similarity 50.0%; Pred. No. 70;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OS Synthetic.

KW Dilated cardiomyopathy absorbents related peptide #1.

XX

DE Dilated cardiomyopathy absorbents related peptide #1.

XX

KW Dilated cardiomyopathy absorbent;

XX

M2 muscarine receptor; antibody.

XX

AC AAM47221;

XX

18-OCT-2001.

XX

Query Match 65.2%; Score 30; DB 4; Length 13;

Best Local Similarity 50.0%; Pred. No. 70;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OS Synthetic.

KW Dilated cardiomyopathy absorbents related peptide #1.

XX

DE Dilated cardiomyopathy absorbents related peptide #1.

XX

KW Dilated cardiomyopathy absorbent;

XX

M2 muscarine receptor; antibody.

XX

AC AAM47221;

XX

18-OCT-2001.

XX

Query Match 65.2%; Score 30; DB 4; Length 13;

Best Local Similarity 50.0%; Pred. No. 70;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OS Synthetic.

KW Dilated cardiomyopathy absorbents related peptide #1.

XX

DE Dilated cardiomyopathy absorbents related peptide #1.

XX

XX (KANF) KANEKA CORP.
 XX PA, Furuyoshi S, Hirai F, Nishimoto T;
 XX PI; 2002-041274/05.
 XX Adsorbents for dilated cardiomyopathy, comprises an immobilized compound
 PT capable of selectively removing antibodies against approximately bi
 PT adrenoceptor and/or M2 muscarine receptors in body fluid without
 PT pretreatment.
 XX PS Claim 3; Page 21; 37pp; Japanese.

XX The present invention relates to a method of immobilising an adsorbent
 CC with a compound capable of binding to an antibody against betal
 CC adrenoceptor and/or an antibody against M2 muscarine receptor on a
 CC water-insoluble support. The adsorbents, apparatus and method are useful
 CC for treating dilated cardiomyopathy by removing antibodies against betal
 CC adrenoceptor and/or M2 muscarine receptor. The present sequence is a
 CC peptide described in the exemplification of the invention

XX Sequence 13 AA;

Query Match 65.2%; Score 30; DB 5; Length 13;
 Best Local Similarity 85.7%; Pred. No. 70;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GSFFSEL 7
 Db 7 GSFFCEL 13

RESULT 10
 AAB86028
 ID AAB86028 standard; peptide; 15 AA.
 AC
 XX DT 12-JUL-2001 (First entry)
 XX DE DCM autoantibody-associated peptide #2.
 KW DCM; autoantibody; betal-adrenergic receptor; dilatative cardiomyopathy;
 KW cardiant; myocardial.
 OS Synthetic.

Key Modified-site 1
 FT /note= "N-terminal acetylated"
 FT Modified-site 15
 FT /note= "C-terminal amide"
 XX PN DE19945210-A1.
 XX PD 29-MAR-2001.
 XX PF 21-SEP-1999; 99DE-01045210.
 XX PR 21-SEP-1999; 99DE-01045210.
 XX PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.
 XX PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
 XX DR WPI; 2001-301258/32.
 XX New autoantibody-binding peptides with an amino acid sequence
 PT corresponding a betal-adrenergic receptor group, useful for treating
 PT dilatative cardiomyopathy.
 XX PS Claim 2; Page 5; 8pp; German.

XX This invention describes novel peptides (1) with an amino acid sequence
 CC corresponding a betal-1-adrenergic receptor group recognized by
 CC autoantibodies associated with dilatative cardiomyopathy (DCM). The
 CC products of the invention have cardiant activity. (1) are useful for
 CC treating DCM by binding autoantibodies directed against myocardial beta-1
 CC -adrenergic receptors, either by neutralizing the antibodies in vivo or
 CC by extracorporeal treatment of blood or plasma with (1) immobilized on a
 CC solid phase. This sequence represents a specifically claimed peptide used
 CC to illustrate the method of the invention
 XX Sequence 15 AA;

Query Match 65.2%; Score 30; DB 4; Length 15;

Query Match 65.2%; Score 30; DB 4; Length 15;
 Best Local Similarity 50.0%; Pred. No. 81;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GSFFSELW 8
 :||:
 3 GTLFSDFW 10

RESULT 11
 AAB86017
 ID AAB86017 standard; peptide; 15 AA.
 AC AAB86017;
 XX DT 12-JUL-2001 (First entry)
 XX DE DCM-associated peptide #17.
 KW DCM; dilatative cardiomyopathy; autoantibody; cardiant;
 KW betal-1 adrenergic activated antibody; immunosuppressive.
 XX OS Synthetic.
 XX Key Modified-site 15
 FT /note= "Lys modified with an amide or free acid group"
 XX FN WO200121660-A1.
 XX PD 29-MAR-2001.
 XX PF 21-SEP-2000; 2000WO-EP009241.
 XX PR 21-SEP-1999; 99EP-00118630.
 XX PR 21-SEP-1999; 99EP-00118631.
 XX PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.
 XX PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
 XX DR WPI; 2001-335469/35.

XX New peptide useful for combating the autoantibodies that are responsible
 PT for dilatative cardiomyopathy.
 XX PS Claim 4; Page 22; 29pp; German.

XX This invention describes a novel peptide (P1) which can be used for (1)
 CC isolating betal-1 adrenergic activated antibodies bound to (P1) on a solid
 CC phase; and (2) a chromatographic apparatus with (P1) bound. The products
 CC of the invention have cardiant and immunosuppressive activity. (P1) is
 CC used to produce medicine to combat beta 1 adrenergic activated
 CC autoantibodies having a causal pathological relationship with dilatative
 CC cardiomyopathy. This sequence represents a specifically claimed peptide
 CC used to illustrate the method of the invention
 XX Sequence 15 AA;

Query Match 65.2%; Score 30; DB 4; Length 15;

PS

Qy	1 GSFFSELM 8 : : 3 GTLFSDFW 10	Pred. No. 81; Best Local Similarity 50.0%; Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;	DT 12-JUL-2001 (first entry)
Db			XX DCM autoantibody-associated peptide #3.
			XX DCM; dilatative cardiomyopathy; beta-1-adrenergic receptor; cardiant; autoantibody; myocardial.
			XX OS Synthetic.
			XX Key Location/Qualifiers
			FT Modified-site 1 /note= "N-terminal acetylated"
			FT Modified-site 15 /note= "C-terminal amide"
			FT PN DE19945211-A1.
			XX XX
			PD 29-MAR-2001.
			XX XX
			PF 21-SEP-1999; 99DE-01045211.
			XX XX
			PR 21-SEP-1999; 99DE-01045211.
			XX XX
			PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.
			XX XX
			PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
			DR WPI; 2001-301259/32.
			XX XX
			PT New antibody-binding peptides with an amino acid sequence corresponding a beta-1adrenergic receptor group useful for treating dilatative cardiomyopathy.
			PT PT
			PT PT
			XX XX
			PS Claim 2; Page 5; 8pp; German.
			XX XX
			CC This invention describes novel peptides (I) with an amino acid sequence corresponding a beta-1-adrenergic receptor group recognized by autoantibodies associated with dilatative cardiomyopathy (DCM). The invention also describes a chromatographic device comprising (I) bound to a solid phase. The products of the invention have cardiant activity. (I) are useful for treating DCM by binding autoantibodies directed against myocardial beta-1-adrenergic receptors, either by neutralizing the antibodies in vivo or by extracorporeal treatment of blood or plasma with (I) immobilized on a solid phase. This sequence represents a specifically claimed peptide used to illustrate the method of the invention
			CC SQ Sequence 15 AA;
			CC Query Match 65.2%; Score 30; DB 4; Length 15;
			CC Best Local Similarity 50.0%; Pre. No. 81;
			CC Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
			CC XX AC AAC020307;
			CC XX DT 31-MAY-2002 (first entry)
			CC DE Human plectin 10 protein N-terminal region.
			CC KW XX
			CC OS Homo sapiens
			CC XX CN1325901-A.
			SQ
			RESUL ^r 14
			AAB86014
			ID AAC020307 standard; peptide; 15 AA.
			XX XX
			AC AC
			XX XX
			DT DT
			XX XX
			DE DE
			KW KW
			OS OS
			XX XX
			PN PN
			VV VV
			RESULT 13
			AAB86022
			ID AAB86022 standard; peptide; 15 AA.
			XX XX

PD 12-DEC-2001.
 XX PS Example 5; Page 18 (Disclosure); 33pp; Chinese.
 CC XX The invention relates to the novel polypeptide-human plectin 10, the
 CC polynucleotide encoding it, the process for preparing the polypeptide by
 CC DNA recombination, the application of the polypeptide in treating
 CC diseases such as cancer and HIV infection. The invention also relates to
 CC the antagonist of the polypeptide and its medical action, and the
 CC application of the polynucleotide. This sequence represents an N-terminal
 CC region of the human plectin 10 protein of the invention
 XX SQ Sequence 15 AA:
 PT Polypeptide-human plectin 10 and polynucleotide encoding it.
 XX PS Example 5; Page 18 (Disclosure); 33pp; Chinese.
 CC XX The invention relates to the novel polypeptide-human plectin 10, the
 CC polynucleotide encoding it, the process for preparing the polypeptide by
 CC DNA recombination, the application of the polypeptide in treating
 CC diseases such as cancer and HIV infection. The invention also relates to
 CC the antagonist of the polypeptide and its medical action, and the
 CC application of the polynucleotide. This sequence represents an N-terminal
 CC region of the human plectin 10 protein of the invention
 XX SQ Sequence 15 AA:
 Query Match 65.2%; Score 30; DB 5; Length 15;
 Best Local Similarity 57.1%; Pred. No. 81;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 SPFSELW 8
 Db 2 AFFSSIW 8

RESULT 15
 ABJ3731
 ID ABJ37231 standard; peptide; 15 AA.
 XX AC ABJ37231;
 XX DT 08-MAY-2003 (First entry)
 XX DE Rhodopsin related G-protein coupled receptor binding site peptide #107.
 XX KW Compound library; microenvironment; G-protein Coupled Receptor; GPCR;
 KW Rhodopsin.
 XX Unidentified.
 XX PN WO2003004147-A2.
 XX 16-JAN-2003.
 XX PD
 XX PR 05-JUL-2002; 2002WO-GB003094.
 XX PR 06-JUL-2001; 2001GB-00016570.
 XX PA (BIOF-) BIOFOCUS PLC.
 XX PI Crossley R, Rose VS, Stevens AP;
 XX DR WPI; 2003-221549/21.
 XX PS Producing compound library, by generating biological target model using
 PT target sequence information, defining microenvironments interacting with
 PT ligand and motifs information, defining microenvironment, and assembling
 PT motifs.
 XX Disclosure; Fig 1; 39pp; English.
 XX The invention relates to a novel method for producing a compound library.
 CC The novel method involves reducing a biological target into a group of

Blank

RESULT 2
US-09-964-821B-53
Sequence 53, Application US/09964821B
Publication No. US20030186360A1
GENERAL INFORMATION:
APPLICANT: FEDER, J. N.
APPLICANT: MINTIER, G.
APPLICANT: RAMANATHAN, C. S.
APPLICANT: HAWKEN, D. R.
APPLICANT: BARBER, L.
APPLICANT: CACACE, A.
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY3,
FILE REFERENCE: D0042NP
CURRENT APPLICATION NUMBER: US/09/964, 821B
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/235, 713
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/261, 783
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/305, 085
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 60/313, 171
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 53
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: polypeptide
US-09-964-821B-53

Query Match Score 28; DB 10; Length 14;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 SFSEELW 8
Db 6 SFSDLW 12

RESULT 3
US-10-268-332-53
Sequence 53, Application US/10268332
Publication No. US20030175748A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY3, EXPRESSED HIGHLY
FILE REFERENCE: D0042A CIP
CURRENT APPLICATION NUMBER: US/10/268, 332
PRIOR APPLICATION NUMBER: 2002-01-10
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: U.S. 60/261, 783
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: U.S. 60/305, 085
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: U.S. 60/313, 171
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: U.S. 09/964, 821
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin version 3.1
SEQ ID NO 53
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-10-268-332-53

Query Match Score 28; DB 14; Length 14;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 SFSEELW 8
Db 6 SFSDLW 12

RESULT 4
US-09-840-085-31
Sequence 31, Application US/09840085
Publication No. US20030165240A1
GENERAL INFORMATION:
APPLICANT: Schehertz Shrader, Alanna
APPLICANT: Chin, Jason W. K.
APPLICANT: Zutshi Reena
APPLICANT: Rutledge, Stacey E.
APPLICANT: Kenibek Martin, Joanne D.
APPLICANT: Zondlo, Neal J.
TITLE OF INVENTION: DNA and Protein Binding Miniature Proteins
FILE REFERENCE: 44574-5099-US
CURRENT APPLICATION NUMBER: US/09/840, 085
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: US 60/199, 408
PRIOR FILING DATE: 2000-04-24
PRIOR APPLICATION NUMBER: US 60/240, 566
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US PROVISIONAL
PRIOR FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US PROVISIONAL
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin ver. 2.1
SEQ ID NO 31
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: p53 miniature
OTHER INFORMATION: protein p53AD
US-09-840-085-31

Query Match Score 27; DB 10; Length 11;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 4 FSEELW 8
Db 3 SFSDLW 7

RESULT 5
US-06-214-371-17
Sequence 17, Application US/09214371B
Publication No. US2001018511A1
GENERAL INFORMATION:
APPLICANT: Lane, David
APPLICANT: Bottger, Volker
APPLICANT: Bottger, Angelica
APPLICANT: Picklesley, Stephen
APPLICANT: Chene, Patrick
APPLICANT: Hochkeppel, Heinz-Kurt
APPLICANT: Garcia-Echeverria, Carlos
APPLICANT: Furet, Pascal
TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2
FILE REFERENCE: 4-20937/A/PCT
CURRENT APPLICATION NUMBER: US/09/214, 371B
PRIOR APPLICATION NUMBER: PCT/EP97/03549
PRIOR FILING DATE: 1997-07-04
NUMBER OF SEQ ID NOS: 83

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-214-371-17

Qy      4 FSELW 8
Db      4 FSDLW 8

RESULT 6
US-09-214-371-24
Sequence 24, Application US/09214371B
Patent No. US20010018511A1
GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Heinz-Kurt
; APPLICANT: Chene, Patrick
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-2093/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SEQ ID NO 24
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence:peptide
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: X = Ac-Gln
; SEQ ID NO 17
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence:peptide
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: Ac-Gln
; LOCATION: (12)
; OTHER INFORMATION: X = Pro-NH2
US-09-214-371-25

Qy      4 FSELW 8
Db      4 FSDLW 8

RESULT 8
US-10-609-217-131
Sequence 131, Application US/10609217
Publication No. US20040044188A1
GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-PA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-227
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/214,371B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/1105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SEQ ID NO 131
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-609-217-131

Qy      4 FSELW 8
Db      4 FSDLW 8

RESULT 7
US-09-214-371-25
Sequence 25, Application US/09214371B
Patient No. US20010018511A1
GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Chene, Stephen
; APPLICANT: Hochkeppel, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-2093/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SEQ ID NO 24
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence:peptide
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: X = Ac-Gln
; SEQ ID NO 17
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence:peptide
; NAME/KEY: VARIANT
; LOCATION: (12)
; OTHER INFORMATION: X = Pro-NH2
; SEQ ID NO 132
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-609-217-132
Sequence 132, Application US/10609217
Publication No. US20040044188A1

```

GENERAL INFORMATION:

APPLICANT: FEIGE, ULRICH
 APPLICANT: LIU, CHUAN-FA
 APPLICANT: CHEETHAM, JANET C.
 APPLICANT: BOONE, THOMAS CHARLES

TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS

FILE REFERENCE: A-527

CURRENT APPLICATION NUMBER: US/10/609,217

CURRENT FILING DATE: 2003-06-27

PRIOR APPLICATION NUMBER: US/09/428,082B

PRIOR FILING DATE: 1999-10-22

PRIOR APPLICATION NUMBER: 60/105,371

PRIOR FILING DATE: 1998-10-23

NUMBER OF SEQ ID NOS: 1133

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 132

LENGTH: 12

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-609-217-132

Query Match 58.7%; Score 27; DB 12; Length 12;
 Best Local Similarity 80.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0;
 Gaps 0;

QY 4 FSBLW 8
 Db 4 FSDLW 8

RESULT 10
US-10-609-217-143

Sequence 143, Application US/10609217

Publication No. US20040044188A1

GENERAL INFORMATION:

APPLICANT: FEIGE, ULRICH
 APPLICANT: LIU, CHUAN-FA
 APPLICANT: CHEETHAM, JANET C.
 APPLICANT: BOONE, THOMAS CHARLES

TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS

FILE REFERENCE: A-527

CURRENT APPLICATION NUMBER: US/10/609,217

CURRENT FILING DATE: 2003-06-27

PRIOR APPLICATION NUMBER: US/09/428,082B

PRIOR FILING DATE: 1999-10-22

PRIOR APPLICATION NUMBER: 60/105,371

PRIOR FILING DATE: 1998-10-23

NUMBER OF SEQ ID NOS: 1133

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 143

LENGTH: 12

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-609-217-143

Query Match 58.7%; Score 27; DB 12; Length 12;
 Best Local Similarity 80.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0;
 Gaps 0;

QY 4 FSBLW 8
 Db 4 FSDLW 8

RESULT 11
US-10-609-217-144

Sequence 144, Application US/10609217

Publication No. US20040044188A1

GENERAL INFORMATION:

RESULT 14
US-10-632-388-143
Sequence 143, Application US/10632388
Publication No. US20040053845A1
GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-FA
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/10/632,388
CURRENT FILING DATE: 2003-07-31
PRIORITY NUMBER: US/09/428,082B
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PatentIn version 3.1
SEQ ID NO 143
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-632-388-142

Query Match Similarity 58.7%; Score 27; DB 12; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FSEIW 8
Db 4 FSDIW 8

RESULT 14
US-10-632-388-143
Sequence 143, Application US/10632388
Publication No. US20040053845A1
GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-FA
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/10/632,388
CURRENT FILING DATE: 2003-07-31
PRIORITY NUMBER: US/09/428,082B
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PatentIn version 3.1
SEQ ID NO 143
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-632-388-143

Query Match Similarity 58.7%; Score 27; DB 12; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FSEIW 8
Db 4 FSDIW 8

RESULT 15
US-10-632-388-144
Sequence 144, Application US/10632388
Publication No. US20040053845A1
GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-FA

APPLICANT: CHEETHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/10/632,388
CURRENT FILING DATE: 2003-07-31
PRIORITY NUMBER: US/09/428,082B
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PatentIn version 3.1
SEQ ID NO 144
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-632-388-144

Query Match Similarity 58.7%; Score 27; DB 12; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FSEIW 8
Db 4 FSDIW 8

Search completed: September 20, 2004, 17:42:42
Job time : 125 secs

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an
k

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 20, 2004, 17:30:00 ; Search time 17 Seconds

(without alignments)
 24.295 Million cell updates/sec

Title: AUDET-SEQ1

Perfect score: 46

Sequence: 1 gffffselw 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:

42678

Minimum DB seq length: 11
 Maximum DB seq length: 15Post-processing: Minimum Match 0%
 Maximum Match 10%
 Listing First 45 summaries

Database : Issued Patents AA:
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 2: /cgm2_6/pctodata/2/iaa/5B_COMB.pep:
 3: /cgm2_6/pctodata/2/iaa/6A_COMB.pep:
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 6: /cgm2_6/pctodata/2/iaa/backtles1.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	30	65.2	11	US-08-424-957-42
2	30	65.2	11	US-09-035-686-43
3	27	58.7	11	US-09-428-082B-131
4	27	58.7	11	US-09-428-082B-132
5	27	58.7	12	US-09-428-082B-143
6	27	58.7	12	US-09-428-082B-144
7	27	58.7	12	US-09-428-082B-144
8	27	58.7	12	US-09-428-082B-144
9	27	58.7	12	US-09-428-082B-144
10	27	58.7	11	US-08-424-957-17
11	27	58.7	11	US-08-424-957-23
12	27	58.7	11	US-08-424-957-24
13	27	58.7	11	US-08-424-957-25
14	27	58.7	11	US-08-424-957-26
15	27	58.7	11	US-08-424-957-26
16	27	58.7	11	US-08-424-957-33
17	27	58.7	11	US-08-424-957-34
18	27	58.7	11	US-08-424-957-36
19	27	58.7	11	US-08-424-957-43
20	27	58.7	11	US-09-035-686-17
21	27	58.7	11	US-09-035-686-23
22	27	58.7	11	US-09-035-686-24
23	27	58.7	11	US-09-035-686-25
24	27	58.7	11	US-09-035-686-25
25	27	58.7	11	US-09-035-686-32
26	27	58.7	11	US-09-035-686-33
27	27	58.7	11	US-09-035-686-34

ALIGNMENTS

RESULT 1
 US-08-424-957-42
 ; Sequence 42, Application US/08424957
 ; Patent No. 5770377
 / GENERAL INFORMATION:
 / APPLICANT: Picklesley, Steven M.
 / INVENTOR: Lane, David P.
 / TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 / TITLE OF INVENTION: Protein and Therapeutic Application Thereof
 / NUMBER OF SEQUENCES: 50
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 / STREET: Four Embarcadero Center, Suite 3400
 / CITY: San Francisco
 / STATE: California
 / COUNTRY: United States
 / ZIP: 94111-4187
 COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patient In Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/424, 957
 / FILING DATE: 19-APR-1995
 / CLASSIFICATION:
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 08/277, 650
 / FILING DATE: 20-JUL-1994
 / ATTORNEY / AGENT INFORMATION:
 / NAME: Dreger, Walter H.
 / REGISTRATION NUMBER: 24,190
 / REFERENCE DOCKET NUMBER: A-6122B/WHD
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (415) 781-1989
 / TELEFAX: (415) 398-3249
 / TELEX: 910 277299
 / INFORMATION FOR SEQ ID NO: 42:
 / SEQUNENCE CHARACTERISTICS:
 / LENGTH: 11 amino acids
 / TYPE: amino acid
 / STRANDEDNESS:
 / TOPOLOGY: unknown
 / US-08-424-957-42
 Query Match 65.2%; Score 30; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 5; Conservative 0; Mismatches 0; Gaps 0;
 Indexes 0;

Qy 4 FSFLW 8

| | | | |
Db 5 FSELW 9

RESULT 2

US-09-035-686-42

; Sequence 42, Application US/09035686

GENERAL INFORMATION:

; APPLICANT: Picklesley, Steven M.

; PATENT NO. 6133391

; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53

; TITLE OF INVENTION: Protein and Therapeutic Application Thereof

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert

; STREET: Four Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: California

; COUNTRY: United States

; ZIP: 94111-4187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/277,660A

; FILING DATE: 20-JUL-1994

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Dreger, Walter H.

; REGISTRATION NUMBER: 24,190

; REFERENCE/DOCKET NUMBER: A-60244/WHD

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989

; TELEFAX: (415) 398-3249

; TELEX: 910 277299

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; US-08-277-660A-9

; RESULT 4

US-08-277-660A-10

; Sequence 10, Application US/08277660A

; Patent No. 5702908

; GENERAL INFORMATION:

; APPLICANT: Bicksley, Steven M.

; APPLICANT: Lane, David P.

; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53

; TITLE OF INVENTION: Protein and Therapeutic Application Thereof

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert

; STREET: Four Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: California

; COUNTRY: United States

; ZIP: 94111-4187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/277,660A

; FILING DATE: 20-JUL-1994

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Dreger, Walter H.

; REGISTRATION NUMBER: 24,190

; REFERENCE/DOCKET NUMBER: A-60244/WHD

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989

; TELEFAX: (415) 398-3249

; TELEX: 910 277299

; INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear

US-08-277-660A-10

Query Match	58.7%	Score: 27;	DB: 1;	Length: 11;
Best Local Similarity	80.0%	Pred. No: 64;		
Matches	4;	Mismatches	1;	Indels
Qy	4 FSELW 8		0;	Gaps 0;
Db	5 FSDLW 9			

RESULT 5
 US-08-277-660A-11
 / Sequence 11, Application US/08277660A
 / Patent No. 5702908

GENERAL INFORMATION:
 APPLICANT: Picklesley, Steven M.

APPLICANT: Lane, David P.

TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 PROTEIN and Therapeutic Application Thereof

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-4187

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/277,660A
 FILING DATE: 20-JUL-1994
 CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-60244/WHD

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEX: 910 277299
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear

US-08-277-660A-12

RESULT 7
 US-08-277-660A-13
 / Sequence 13, Application US/08277660A
 / Patent No. 5702908

GENERAL INFORMATION:
 APPLICANT: Picklesley, Steven M.

APPLICANT: Lane, David P.

TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 PROTEIN and Therapeutic Application Thereof

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-4187

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/277,660A
 FILING DATE: 20-JUL-1994
 CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Walter H.

Query Match

Qy	4 FSELW 8	Score: 27;	DB: 1;	Length: 11;
Db	5 FSDLW 9	Pred. No: 64;		
Qy	4 FSELW 8	1;	Indels 0;	Gaps 0;
Db	5 FSDLW 9			

RESULT 6
 US-08-277-660A-12
 / Sequence 12, Application US/08277660A
 / Patent No. 5702908

GENERAL INFORMATION:
 APPLICANT: Picklesley, Steven M.

REGISTRATION NUMBER: 24,190
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEX: (415) 398-3249
 INFORMATION OR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-277-660A-13

Query Match 58.7%; Score 27; DB 1; Length 11;
 Best Local Similarity 80.0%; Pred. No. 64;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FSEIW 8
 Db 5 FSIDLW 9

RESULT 8
 US-08-277-660A-19
 Sequence 19, Application US/08277660A
 Patent No. 5702908

GENERAL INFORMATION:
 APPLICANT: Picklesley, Steven M.
 APPLICANT: Lane, David P.
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 TITLE OF INVENTION: Protein and Therapeutic Application Thereof
 NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-4187

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/277,660A
 FILING DATE: 20-JUL-1994

CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Walter H.
 REGISTRATION NUMBER: 24,190
 REFERENCE/DOCKET NUMBER: A-60244/WHD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 APPLICATION NUMBER: US/08/277,660A
 FILING DATE: 20-JUL-1994

CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Walter H.
 REGISTRATION NUMBER: 24,190
 REFERENCE/DOCKET NUMBER: A-60244/WHD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 APPLICATION NUMBER: US/08/277,660A
 FILING DATE: 20-JUL-1994

SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 STRANDEDNESS:
 TOPOLOGY: linear
 ZIP: 94111-4187

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

RESULT 9
 US-08-277-660A-20
 Sequence 20, Application US/08277660A
 Patent No. 5702908

GENERAL INFORMATION:
 APPLICANT: Picklesley, Steven M.
 APPLICANT: Lane, David P.
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 TITLE OF INVENTION: Protein and Therapeutic Application Thereof
 NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-4187

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

Query Match 58.7%; Score 27; DB 1; Length 11;
 Best Local Similarity 80.0%; Pred. No. 64;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FSEIW 8
 Db 5 FSIDLW 9

RESULT 10
 US-08-424-957-17
 Sequence 17, Application US/08424957
 Patent No. 5770377

GENERAL INFORMATION:
 APPLICANT: Picklesley, Steven M.
 APPLICANT: Lane, David P.
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 TITLE OF INVENTION: Protein and Therapeutic Application Thereof
 NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-4187

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

Query Match 58.7%; Score 27; DB 1; Length 11;
 Best Local Similarity 80.0%; Pred. No. 64;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FSEIW 8
 Db 5 FSIDLW 9

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// SOFTWARE: PatentIn Release #1.0, Version #1.30
// CURRENT APPLICATION DATA:
// APPLICATION NUMBER: US/08/424, 957
// FILING DATE: 19-APR-1995
// CLASSIFICATION:
// PRIORITY APPLICATION DATA:
// APPLICATION NUMBER: US 08/277, 660
// FILING DATE: 20-JUL-1994
// ATTORNEY/AGENT INFORMATION:
// NAME: Dreger, Walter H.
// REGISTRATION NUMBER: 24,190
// TELECOMMUNICATION INFORMATION:
// TELEPHONE: (415) 781-1989
// TELEX: 910 277299
// INFORMATION FOR SEQ ID NO: 17:
// SEQUENCE CHARACTERISTICS:
// LENGTH: 11 amino acids
// TYPE: amino acid
// STRANDEDNESS: unknown
// US -08-424-957-17

Query Match 58.7%; Score 27; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FSELW 8
Db 5 FSDLW 9

RESULT 12
US-08-424-957-24
; Sequence 24, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Lane, David P.
; ATTORNEY: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424, 957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277, 660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE DOCKET NUMBER: A-61228/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US -08-424-957-24

Query Match 58.7%; Score 27; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FSELW 8
Db 5 FSDLW 9

RESULT 13
US-08-424-957-25
; Sequence 25, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
;
```

APPLICANT: Picklesley, Steven M.
 ATTICANT: Lane, David P.
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-4187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/424,957
 FILING DATE: 19-APR-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/277,660
 FILING DATE: 20-JUL-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Walter H.
 REGISTRATION NUMBER: 24,190
 REFERENCE/DOCKET NUMBER: A-61228/WHD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 TELEX: 910 277299
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 US-08-424-957-25

Query Match 58.7%; Score 27; DB 1; Length 11;
 Best Local Similarity 80.0%; Pred. No. 64;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FSELW B
 Db 5 FSDLW 9

RESULT 15
 US-08-424-957-32
 Sequence 32; Application US/08424957
 Patent No. 5770377
 GENERAL INFORMATION:
 APPLICANT: Picklesley, Steven M.
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, David P.
 REGISTRATION NUMBER: 24,190
 REFERENCE/DOCKET NUMBER: A-61228/WHD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 TELEX: 910 277299
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 US-08-424-957-25

Query Match 58.7%; Score 27; DB 1; Length 11;
 Best Local Similarity 80.0%; Pred. No. 64;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FSELW B
 Db 5 FSDLW 9

RESULT 14
 US-08-424-957-26
 Sequence 26; Application US/08424957
 Patent No. 5770377
 GENERAL INFORMATION:
 APPLICANT: Picklesley, Steven M.
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, David P.
 REGISTRATION NUMBER: 24,190
 REFERENCE/DOCKET NUMBER: A-61228/WHD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 TELEX: 910 277299
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown

Tue Sep 21 08:51:50 2004

audet-seq1.szlm.rai

Page 7

US-08-424-957-32

Query Match 58.7%; Score 27; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSEIW 8
 | : ||
Db 5 FSDLW 9

Search completed: September 20, 2004, 17:32:33
Job time : 18 secs

B
I
A
N
T

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2004, 17:28:40 ; Search time 36 Seconds
(without alignments)
70.115 Million cell updates/sec

Title: AUDET-SEQ1
Perfect score: 46
Sequence: 1 gsfFfSelw B

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315516202 residues

Total number of hits satisfying chosen parameters: 2511

Minimum DB seq length: 11
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:
 1: sp_archea:
 2: sp_bacteria:
 3: sp_fungi:
 4: sp_human:
 5: sp_invertebrate:
 6: sp_mammal:
 7: sp_mhc:
 8: sp_organelle:
 9: sp_phage:
 10: sp_plant:
 11: sp_rabbit:
 12: sp_virus:
 13: sp_vertebrate:
 14: sp_unclassified:
 15: sp_rvirus:
 16: sp_bacteriophage:
 17: sp_archaea:
 18: sp_bacteria:
 19: sp_fungi:
 20: sp_invertebrate:
 21: sp_mammal:
 22: sp_mhc:
 23: sp_organelle:
 24: sp_phage:
 25: sp_plant:
 26: sp_rabbit:
 27: sp_virus:
 28: sp_vertebrate:
 29: sp_unclassified:
 30: sp_rvirus:
 31: sp_bacteriophage:
 32: sp_bacteria:
 33: sp_fungi:
 34: sp_invertebrate:
 35: sp_mammal:
 36: sp_mhc:
 37: sp_organelle:
 38: sp_phage:
 39: sp_plant:
 40: sp_rabbit:
 41: sp_virus:
 42: sp_vertebrate:
 43: sp_unclassified:
 44: sp_rvirus:
 45: sp_bacteriophage:

ALIGNMENTS

RESULT 1
ID: 077896 PRELIMINARY;
AC: 077896; CREATED
DT: 01-NOV-1998 (TREMBLrel); 08, Created
DT: 01-DEC-2001 (TREMBLrel); 08, Last sequence update
DE: MHC class II B locus 12 (Fragment)
OS: Oreochromis niloticus (Nile tilapia)
EU: Metazoa; Chordata; Craniota; Buteleostomi;
OC: Actinopterygii; Neopterygii; Teleostei; Buteleosteoi; Neoteleosteoi;
OC: Acanthomorpha; Acanthopterygii; Perciformes; Labroidei;
OC: Cichlidae; Oreochromis.
NCBI_TaxID=8128;

[1]
RN PREQUENCE FROM N.A., PubMed=9649539;
RP MEDLINE:98315113; PubMed=9649539;
RX Malaga-Trillo B., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueiroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotye polymorphism among cichlid mhc
class II B loci";
RT GenBank 149:1527-1537(1998).
DR TMBL; AF050006; AAC41345.1; -.
FT NON_TER 1 1
FT NON_TER 11 1399 MW; 3F47DB7A772685A3 CRC64;
SQ SEQUENCE 11 AA; 1399 MW;

Query Match 52.2%; Score 24; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 4; Se+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 FFSEELW 8
Db 3 FWSMLN 8

RESULT 2
ID: P83537 PRELIMINARY;

Result No.	Score	Match	Length	DB	ID	Description
1	24	52.2	11	7	077896	077896 oreochromis
2	23	50.0	11	2	P83537	P83537 lactobacillus
3	23	50.0	11	7	077895	077895 oreochromis
4	23	50.0	13	8	Q9XL12	Q9XL12 bennisa tab
5	23	50.0	15	2	Q9R5D6	Q9R5D6 chromatin
6	22	47.8	12	6	Q9TRT7	Q9TRT7 bos taurus
7	20	43.5	11	7	077898	077898 oreochromis
8	20	43.5	11	7	077894	077894 oreochromis
9	19	41.3	12	6	Q46664	Q46664 macrospiro
10	19	41.3	11	4	Q9UC46	Q9UC46 homo sapien
11	19	41.3	12	2	Q53579	Q53579 rhodobacter
12	19	41.3	13	5	Q812E2	Q812E2 plasmidium
13	19	41.3	15	2	Q47892	Q47892 firmicilla d
14	19	41.3	15	2	Q53580	Q53580 rhodobacter
15	19	41.3	15	2	Q47893	Q47893 firmicilla d
16	19	41.3	15	11	Q92398	Q92398 rattus norvegicus

OS Bos taurus (Bovine). Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TAXID=9913;
 RN [1] _
 RP SEQUENCE.
 RX MEDLINE=92132498; PubMed=1734497;
 RA Veiby O.P., Sletten K., Husby G., Nordsgaard K.;
 RT "Amino acid sequence analyses of non-AA proteins from amyloid fibrils
 of bovine kidney.";
 RL Scand. J. Immunol. 35:63-69(1992).
 FT NON_TER 1 1
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1503 MW; 64CDB543C6D4AEB CRC64;
 Query Match Score 22; DB 6; Length 12;
 Best Local Similarity Pred. No. 1.2e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 SFPSSELW 8
 Db 1 SFPEXXYY 7

RESULT 7
 ID 077898 PRELIMINARY; PRT; 11 AA.
 AC 077898; Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MHC class II B locus 12 (Fragment).
 DE Macropterus robustus.
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 AC Actinopterygii; Neopterygii; Teleostei; Euteleosteoi; Neoteleosteoi;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidei;
 OC Cichlidae; Oreochromis.
 OX NCBI_TAXID=8128;
 RN [1] _
 RP SEQUENCE FROM N.A. MEDLINE=98315113; PubMed=9649539;
 RX Malaga-Trillo B., Zaleska-Rutczynska Z., McAndrew B., Vinczek V.,
 RA Figueiroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 class II loci.";
 RL Genetics 149:1527-1537(1998).
 DR AF050004; AAC41343.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1367 MW; 3F47DC0A62C045A3 CRC64;
 Query Match Score 20; DB 7; Length 11;
 Best Local Similarity Pred. No. 2.9e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 FFSELW 8
 Db 3 FWSIVW 8

RESULT 8
 ID 077894 PRELIMINARY; PRT; 11 AA.
 AC 077894; Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Neurophil inhibitor peptide, NIP-POLYMORPHONUCLEAR neutrophil
 DE inhibitor peptide.
 OS Homo sapiens (Human).
 OC Butarizota; Merazoa. Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TAXID=9606;
 RN [1] _
 RP SEQUENCE.

RESULT 9
 ID 046664 PRELIMINARY; PRT; 12 AA.
 AC 046664; Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-JUN-1998 (TREMBLrel. 06, Last annotation update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Glucosidase-6-phosphate dehydrogenase (fragment).
 DE GPD.
 OS Macropterus robustus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 OX NCBI_TAXID=55580;
 RN [1] _
 RP SEQUENCE FROM N.A. MEDLINE=9724585; PubMed=9060417;
 RX Loebel D.A., Johnston P.G.;
 RA RT "Analysis of the intron-exon structure of the G6PD gene of the
 wallaroo (Macropus robustus) by polymerase chain reaction.";
 RL Genome 8:146-147(1997).
 DR FMBI; IIS3774; AAC48789.1; -.
 FT NON_TER 1 1
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1430 MW; D42A9CB4E3CB1AA9 CRC64;
 Query Match Score 20; DB 6; Length 12;
 Best Local Similarity Pred. No. 3.1e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 10
 ID Q9UC46 PRELIMINARY; PRT; 11 AA.
 AC Q9UC46; Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Neurophil inhibitor peptide, NIP-POLYMORPHONUCLEAR neutrophil
 DE inhibitor peptide.
 OS Homo sapiens (Human).
 OC Butarizota; Merazoa. Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TAXID=9606;
 RN [1] _
 RP SEQUENCE.

Query Match Score 19; DB 4; Length 11;
Best Local Similarity 75.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSFF 4
DB 3 GSYF 6

RESULT 11
ID Q53579 PRELIMINARY; PRT; 12 AA.
AC Q53579;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Light harvesting complex I alpha polypeptide (Fragment).
GN pufA.
OS Rhodobacter capsulatus (Rhodopseudomonas capsulata).
OC Bacteria; Proteobacteria; Alpha proteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92234363; PubMed=1563029;
RT "Characterization of LHI- and LHI+ Rhodobacter capsulatus pufA mutants".
RT J. Bacteriol. 174:3030-3041 (1992).
DR EMBL; S97551; AAC60405.1;
FT NON TER 12 12
SEQUENCE 12 AA; 1627 MW; 0F92F6EABA70532B CRC64;

Query Match Score 19; DB 2; Length 12;
Best Local Similarity 42.9%; Pred. No. 5e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 SFFSEIWN 8
DB 2 SKFYKWW 8

RESULT 12
ID Q812E2 PRELIMINARY; PRT; 13 AA.
AC Q812E2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE Hypothetical protein (Fragment).
GN PFA0655W.
OS Plasmodium falciparum (isolate 3D7).
OC Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36529;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22255708; PubMed=12368867;
RA Hall N., Pain A., Berri M., Churcher C., Harris B., Harris D.,
RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser R., Hornsby T., Holroyd S., Horrocks P.,

RA Humphrey S., Jagels K., James K.D., Johnson D., Kerhoornou A.,
RA Knights A., Konforov B., Kyes S., Larre N., Lawson D., Leonard N.,
RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitzch E.,
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M.,
RA Seeger K., Sharp S., Smith R., Squares R., Stevens K.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sulston J.E., Craig A., Newbold C., Barrell B.G.;
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
RL Nature 419:527-531 (2002).
DR EMBL; AL031744; CAD48947.1; -.
KW Hypothetical protein.
FT NON TER 1 1
SQ SEQUENCE 13 AA; 1619 MW; 50E352E2F7FED1A7 CRC64;

Query Match Score 19; DB 5; Length 13;
Best Local Similarity 60.0%; Pred. No. 5.4e+03;
Matches 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SFFSEI 6
DB 7 TFYSE 11

RESULT 13
ID Q47892 PRELIMINARY; PRT; 15 AA.
AC Q47892;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Beta-allophycocyanin (Fragment).
OS Fremyella diplosiphon (Calothrix) RCC 7601.
OC Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Fremyellales;
NCBI_TaxID=1197;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86233345; PubMed=3086870;
RA Conley P.B., Lemieux P.G., Lomax T.L., Grossman A.R.;
RT "Genes encoding major light-harvesting polypeptides are clustered on
the genome of the cyanobacterium Fremyella diplosiphon.";
RT Proc. Natl. Acad. Sci. U.S.A. 83:3924-3928 (1986).
DR EMBL; M13216; AAA24871.1; -.
FT NON TER 1 1
SQ SEQUENCE 15 AA; 1644 MW; 97221656699F462F CRC64;

Query Match Score 19; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSFF 4
DB 4 GSYF 7

RESULT 14
ID Q53580 PRELIMINARY; PRT; 15 AA.
AC Q53580;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Light-harvesting complex I alpha polypeptide (Fragment).
GN PUFA.
OS Rhodobacter capsulatus (Rhodopseudomonas capsulata).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1661;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92234963; PubMed=1569029;
RA Richter P., Brand M., Drews G.;
RA Characterization of LHI- and LHI+ Rhodobacter capsulatus pufA.

RT mutants.";
 RL J. Bacteriol. 174:3030-3041 (1992).
 DR EMBL; S97532; AAC6046.1; -.
 PT NON-TER 15 15
 SQ SEQUENCE 15 AA; 2054 MW; 3561FE413591D31A CRC64;
 Query Match 41.3%; Score 19; DB 2; Length 15;
 Best Local Similarity 42.9%; Pred. No. 6.3e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 SFPSSELW 8
 Db 2 SKFYKIV 8

RESULT 15

Q47893 PRELIMINARY; PRT; 15 AA.
 ID Q47893
 AC Q47893;
 DT 01-NOV-1996 (TREMBrel. 01, Created)
 DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBrel. 08, Last annotation update)
 DE Beta-phycocyanin (Fragment).
 OS Fremyella diplosiphon (Calothrix PCC 7601).
 OC Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Fremyella.
 OX NCBI_TaxID=1197;
 RN [1]
 RP SEQUENCE FROM N.A. MEDLINE=86233345; PubMed=3086870;
 RX Conley B.B., Lemaux P.G., Lomax T.L., Grossman A.R.;
 RT "Genes encoding major light-harvesting polypeptides are clustered on
 the genome of the cyanobacterium Fremyella diplosiphon."
 RT Proc. Natl. Acad. Sci. U.S.A. 83:3924-3928 (1986).
 DR EMBL; M13217; AAA24880.1; -.
 PT NON-TER 1 1
 SQ SEQUENCE 15 AA; 1528 MW; 7FF2F6551.8F493D4 CRC64;
 Query Match 41.3%; Score 19; DB 2; Length 15;
 Best Local Similarity 75.0%; Pred. No. 6.3e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GSFF 4
 Db 4 GSYF 7

Search completed: September 20, 2004, 17:31:51
 Job time : 38 secs

Blank

Scoring table:	BLOSUM62	34	13	28.3	13	1	YPNP_PHLUJ
	Gapop 10.0 , Gapext 0.5	35	13	28.3	14	1	LPF2_ECOLI
Searched:	141681 seqs, 52070155 residues	35	13	28.3	14	1	P18854_rhizobium_m
Total number of hits satisfying chosen parameters:	430	36	13	28.3	14	1	P86985_escherichia
Minimum DB seq length:	11	37	13	28.3	14	1	P86939_periplaneta
Maximum DB seq length:	15	38	13	28.3	14	1	P82750_myxocephal
Post-processing:	Minimum Match 0%	39	13	28.3	14	1	P31885_alligator_m
	Maximum Match 100%	40	13	28.3	14	1	P81362_lactistridium
Database :	Swissprot_42:*	41	13	28.3	15	1	P83057_escherichia
Perfect score:	46	42	13	28.3	15	1	P36522_saccharomyces_cerevisiae
Sequence:	1 gsfFseIw 8	43	13	28.3	15	1	P80620_tea_mays_m
		44	13	28.3	15	1	P80634_tea_mays_m
Title:	AUDET-SEQ1	45	12.5	27.2	12	1	P35490_scyllophorus_aeneus
ALIGNMENTS							
Scoring table:	BLOSUM62	RESULT 1					
	Gapop 10.0 , Gapext 0.5	NP3_LYMST	ID	NP3_LYMST	STANDARD;	PRT;	13 AA.
Searched:	141681 seqs, 52070155 residues	AC	P80180;				
Total number of hits satisfying chosen parameters:	430	DT	01-JUL-1993 (Rel. 26, Created)				
Minimum DB seq length:	11	DT	01-JUL-1993 (Rel. 26, Last sequence update)				
Maximum DB seq length:	15	DT	01-JUL-1993 (Rel. 26, Last annotation update)				
Post-processing:	Minimum Match 0%	DE	Lymnaea-ds-amide 3.				
	Maximum Match 100%	OS	Lymnaea stagnalis (Great pond snail).				
Database :	Swissprot_42:*	OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora; Lymnaeoidea; Lymnaeidae; Lymnaea.				
Perfect score:	46	OX	[1] NCBI_TaxID=6523;				
Sequence:	1 gsfFseIw 8	RN					
		RP					
		RC	SEQUENCE.				
		RC	TISSUE-Ganglion;				
		RX	PubMed-93238777; PubMed-8477756;				
		RX	Medline-93238777; PubMed-8477756;				
		RA	Johnsen A.H.; Rehfeld J.F.;				
		RT	"Lymnaepramides", a new family of neuropeptides from the pond snail.				
		RT	Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in				
		RT	invertebrates?";				
		RT	Eur. J. Biochem. 213:875-879(1993).				
		RL	CC-1-SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.				
		DR	DR S32473; S32473.				
		KW	Neuropeptide; Amidation.				
		FT	FT MOD RES 13 13 AMIDATION.				
		FT	FT UNSURE 12 12				
		SQ	SQ SEQUENCE 13 AA; 1462 MW; 9CA07BA3F5D5B865 CRC64;				
		Query Match	Query Match Score 20; DB 1; Length 13;				
		Best Local Similarity	Best Local Similarity 66.7%; Pred. No. 5.e+02;				
		Matches	Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;				
		Qy	Qy 1 GSFFFS 6				
		Db	Db 7 GSAFSD 12				
		RESULT 2					
		ALB2_TRASC	ID ALB2_TRASC STANDARD;				
		AC	AC P81189; Rel. 36, Created)				
		DT	DT 15-JUL-1998 (Rel. 36, Last sequence update)				
		DT	DT 15-JUL-1998 (Rel. 41, Last annotation update)				
		DE	DE 68 kDa Serum albumin (Alb-2) (Fragment).				
		OS	OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).				
		OC	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;				
		OC	OC Testudinoidea; Emydidae; Trachemys.				
		NCBI_TaxID=3403;	[1]				
		RN	RN SEQUENCE.				
		RX	RX MEDLINE-940230; PubMed-9440230;				
		RA	RA Brown M.A.; Chambers G.K., Licht P.;				
		RT	RT Purification and partial amino acid sequences of two distinct				
		RT	RT albums from turtle plasma. ";				
		RL	RL Comp. Biochem. Physiol. 118B:367-374 (1997).				

CC -!- FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K+, fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Plasma.

CC -!- MISCELLANEOUS: In the red-eared slider turtle, there are two forms of albumin, ALB-1 and ALB-2.

CC -!- SIMILARITY: Belongs to the ALB/AFP/VDB family.

DR Intero; IPR000264; ALBUMIN; PARTIAL.

KW PROSTET; PS00212; ALBUMIN; PARTIAL.

FT NON-TER 15 15

SEQUENCE 15 AA; 1733 MW; 4B7422B89FF73223 CRC64;

Query Match Score 19; DB 1; Length 15;
Best Local Similarity 57.1%; Pred. No. 9.6e-02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GSFFSEED 7
Db 9 GHXFXEL 15

RESULT 3

LPW THETH LPW THETH STANDARD; PRT; 11 AA.

AC P05544;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)

DB Trp operon leader peptide.

GN TRPL.

CQ Thermus thermophilus.

CC Bacteries; Deinococcus-Thermus; Deinococci; Thermales; Thermacae;

CC Thermus.

NCBI_TAXID=274;
RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=HB8 / ATCC 27634;

RA MEDLINE=89000781; PubMed=2844259;

RA Sato S., Nakada Y., Kanaya S., Tanaka T.;
RT "Molecular cloning and nucleotide sequence of Thermus thermophilus
HB8 trpB and trpG.";
RL Biophys. Acta 950:303-312 (1988).

CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS OF TRYPTOPHAN.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR EMBL; X0744; CAA30565.1; -.

KW TRYPTOPHAN biosynthesis; Leader peptide.

SEQUENCE 11 AA; 1228 MW; 364B295A772DC5A7 CRC64;

Query Match Score 18; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 SELW 8
Db 5 SALW 8

RESULT 4

TNNA SCYCA STANDARD; PRT; 11 AA.

ID TNNA_SCYCA
AC P41333;

Query Match	39.1%; Score 18; DB 1; Length 15;	FT	.10D RES	12 AA;	12	AMIDATION.
Best Local Similarity	50.0%; Pred. No. 1.5e+03;	SQ	SEQUENCE	12 AA;	1383 MW;	31209192EF49D777 CRC64;
Matches	3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	Query Match	34.0%; Score 16; DB 1; Length 12;			
Qy	1 GSFFSE 6	Best Local Similarity	75.0%; Pred. No. 2.9e+03;	0; Mismatches 1; Indels 0;	Gaps 0;	
Db	5 GBFLAE 10	Matches	3; Conservative 0;			
<hr/>						
RESULT 6		Qy	1 GSFF 4			
MHBI KLEPN	STANDARD;	Db	9 GSIF 12			
ID MHBI KLEPN	PRT; 11 AA.					
AC P80580;						
DT 01-OCT-1996 (Rel. 34, Created)		RESULT 8				
DT 01-OCT-1996 (Rel. 34, Last sequence update)		UP001 CAEEL	STANDARD;	PRT;	12 AA.	
DT 01-NOV-1997 (Rel. 35, Last annotation update)		ID UP001 CAEEL				
DE Maleylpyruvate isomerase (EC 5.2.1.4) (Fragment).		AC P55954;				
GN		DT 01-NOV-1997 (Rel. 35, Last sequence update)				
OS Klebsiella pneumoniae.		DT 01-NOV-1997 (Rel. 35, Last annotation update)				
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;		DE Unknown protein from 2D-page (Spot 1) (Fragment).				
OC Enterobacteriaceae; Klebsiella.		OS Caenorhabditis elegans.				
NCBI_TaxID=573;		OC Cukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;				
[1]		OC Rhabditidae; Peioderinae; Caenorhabditis.				
RN		NCBI_TaxID=6239;				
RP		[1]				
SEQUENCE:		RN SEQUENCE.				
RX MEDLINE=96349117; PubMed=9760924;		RC STRAIN=Bristol N2;				
RA Robson N.D., Parrott S., Cooper R.A.;		RX MEDLINE=9795299; PubMed=9150941;				
RT "In vitro formation of a catabolic plasmid carrying Klebsiella		RA Bini L., Heid H., Liberatore S., Pallini V., Zwilling R.;				
RT pneumoniae DNA that allows growth of Escherichia coli K-12 on 3-		RT "Two-dimensional gel electrophoresis of Caenorhabditis elegans				
RT hydroxybenzoate."		RT homogenates and identification of protein spots by microsequencing.";				
RL Microbenzoylbenzoate."		RL Electrophoresis 18:557-562(1997).				
CC -1-CATALYTIC ACTIVITY: 3-maleylpyruvate = 3-fumarylpyruvate.		DR Siena-2DPAGE; P55954; -.				
KW Isomerase.		FT NON-TER 12 AA; 12				
FT NON TER 11 AA; 11 MW; 1EE0E2DD49C9DSAB CRC64;		SQ SEQUENCE 12 AA; 1409 MW; 8D04A7105316905A CRC64;				
SEQUENCE 11 AA;						
Query Match	37.0%; Score 17; DB 1; Length 11;					
Best Local Similarity	75.0%; Pred. No. 1.7e+03;	Query Match	34.8%; Score 16; DB 1; Length 12;			
Matches	3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity	37.5%; Pred. No. 2.9e+03;			
Qy	2 SFFS 5	Matches	0; Mismatches 5; Indels 0; Gaps 0;			
Db	5 SFPN 8	Qy	1 GSFFSELW 8			
<hr/>						
RESULT 7		Db 3 GDDIMEKW 10				
FAR7_PENMO	STANDARD;					
ID FAR7_PENMO	PRT; 12 AA.					
AC P83322;		RESULT 9				
DT 28-FEB-2003 (Rel. 41, Created)		CXAI CONCN	STANDARD;	PRT;	14 AA.	
DT 28-FEB-2003 (Rel. 41, Last sequence update)		ID CXAI CONCN				
DT 28-FEB-2003 (Rel. 41, Last annotation update)		AC P56973;				
DE FMRFamide-like neuropeptide FLP7 (GYRKPFPNSIF-amide).		DT 16-OCT-2001 (Rel. 40, Created)				
DE Penaeus monodon (Penaeo shrimp).		DT 16-OCT-2001 (Rel. 40, Last sequence update)				
OS Eukaryota; Arthropoda; Crustacea; Malacostraca;		DT 28-FEB-2003 (Rel. 41, Last annotation update)				
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;		DE Alpha-conotoxin CnIB.				
OC Penaeidae; Penaeus.		OS Corus consors (Singed cone).				
NCBI_TaxID=6687;		OC Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;				
RN		OC Apogastropoda; Caenogastropoda; Sorboconcha; Hypsogastropoda;				
RP SEQUENCE, AND MASS SPECTROMETRY.		OC Neogastropoda; Conidae; Conidae; Comus.				
RC TISSUE=Eye stalk;		NCBI_TaxID=101297;				
RC MEDLINE=21956277; PubMed=111959015;		RN SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND STRUCTURE BY NMR.				
RA Sithigorngul P., Pippen J., Krungrasem C., Longrant S.,		RC TISSUE=Venom;				
RA Chaivitsathangkura P., Sithigorngul W., Petson A.;		MEDLINE=9255390; PubMed=10320362;				
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk		RA Favreau P., Kriemann I., Le Gall F., Bobenreith M.J., Lamthanh H.,				
RT of the giant tiger prawn Penaeus monodon."		RA Bouet F., Servent D., Molgo J., Menez A., Letourneux Y.,				
RL Comp. Biochem. Physiol. 131B:325-337 (2002).		RA Lancevin J.-M.;				
CC -1- SUBCELLULAR LOCATION: Secreted.		RT "Biochemical characterization and nuclear magnetic resonance				
CC -1- MASS SPECTROMETRY: MW=1381.4; METHOD=MALDI.		RT structure of novel alpha-conotoxins isolated from the venom of Comus				
CC -1- SIMILARITY: Belongs to the FMRFamide-related peptide family.		RT consors."				
CC GO: GO:0007218; P:Neuropeptide signaling pathway; TAS.		RL Biochemistry 38:6117-6126(1999).				
KW Neuropeptide; Amidation.		CC -1- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they bind to the nicotinic acetylcholine receptors (nAChR) and thus inhibit them. This peptide seems to be a potent and selective blocker of muscular subtype of nAChR.				

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
 family.
 CC PIR: A58963; A58963.
 DR PDB: 1B45; 09-JUL-99.
 KW Post-synaptic neurotoxin; Neurotoxin; Toxin;
 Acetylcholine receptor inhibitor; Amidation; 3D-structure.
 FT PEPTIDE 1 14 ALPHA-CONOTOXIN CNIA.
 FT PEPTIDE 3 14 ALPHA-CONOTOXIN CNIB.
 FT DISULFID 3 8
 FT DISULFID 4 14
 FT MOD RES 14 14 AMIDATION.
 FT HELIX 6 8
 FT TURN 9 10
 SQ SEQUENCE 14 AA; 1548 MW; D3EE9196B5E5BD CRC64;
 Query Match 34.8%; Score 16; DB 1; Length 14;
 Best Local Similarity 40.0%; Pred. No. 3.3e+03;
 Matches 2; Conservative 2; Mismatches 0; Gaps 0;
 QY 1 GSFFS 5
 DB 9 GKYY 13
 RESULT 10
 FIBA_HORSE STANDARD; PRT; 14 AA.
 ID FIBA_HORSE
 AC P14452;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-2003 (Rel. 13, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Fibrinogen alpha chain [Contains: Fibronopeptide A] (Fragment).
 GN FGA.
 OS EQUUS caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 NCBI_TaxID=9736;
 RN SEQNCE.
 RP Blomback B., Blomback M., Grondahl N.J.;
 RT "Studies on fibrinopeptides from mammals.";
 RL Acta Chem. Scand. 19:1759-1794(1965).
 CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
 polymerize into fibrin and acting as a cofactor in platelet
 aggregation.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 which cleaves fibrinopeptides A and B from alpha and beta chains,
 and thus exposes the N-terminal polymerization sites responsible
 for the formation of the soft clot.
 KW Blood coagulation; Plasma.
 FT PEPTIDE 1 14 FIBRINOPEPTIDE A.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1517 MW; 4E998EB63C2A15E7 CRC64;
 Query Match 34.8%; Score 16; DB 1; Length 14;
 Best Local Similarity 50.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GSFFSE 6
 DB 4 GEFLME 9
 RESULT 12
 CA42_LITCI STANDARD; PRT; 11 AA.
 ID CA42_LITCI
 AC P82052;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DB Caerulein 4.2/4.2/4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Peledrydiniae; Litoria.
 NCBI_TaxID=94170;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=2005701; PubMed=1059099;
 RA Walnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue

mountains tree frog *Litoria citropa*. Part 1. Sequence determination using electrospray mass spectrometry.";

Rapid Commun. Mass Spectrom. 13:2498-2502 (1999).

-!- FUNCTION: Hypotensive neuropeptide (Probable).

-!- SUBCELLULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: Skin dorsal glands.

-!- PTM: Isoform 4.2X4 differs from isoform 4.2 in not being sulfated.

CC -!- MASS SPECTROMETRY: MW=1404; METHOD=Electrospray.

CC : SIMILARITY: Belongs to the gastrin/cholecystokinin family.

DR Interpro: IPR001651; Gastrin.

DR PROSITE: PS00259; GASTRIN; FALSE NEG.

KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;

KW Pyrrolidone carboxylic acid.

FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD RES 4 4 SULFATION.

FT MOD RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1344 NW; 10DABB94F5B8861BB CRC64;

Query Match 32.6%; Score 15; DB 1; Length 11;

Best Local Similarity 75.0%; Pred. No. 4e+03; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSFF 4

DB 6 GSHP 9

RESULT 13

ID CXA2_CONGE ID KARA_BROPL STANDARD; PRT; 13 AA.

AC P01520; ID KARA_BROPL STANDARD; PRT; 13 AA.

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Alpha-conotoxin GI.

OS Conus geographus (Geography cone).

OC Bivalvia; Mollusca; Gastropoda; Orthogastropoda;

OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;

OC Neogastropoda; Conoidea; Conidae; Conus.

NCBI_TaxID=6491; [1]

RP SEQUENCE.

RX MEDLINE=81191854; PubMed=7014556;

RA Gray W.R., Luque A., Olivera B.M., Barrett J., Cruz L.J.; RT "Peptide toxins from *Conus geographus* venom.";

RL J. Biol. Chem. 256:4734-4740(1981).

RN [2]

RP DISULFIDE BONDS.

RX MEDLINE=84280842; PubMed=6466616;

RA Gray W.R., Luque F.A., Galvean R., Atherton E., Sheppard R.C., Stone B.L., Reyes A., Alföldi J., McIntosh M., Olivera B.M., Cruz L.J., Rivier J.

RA "Conotoxin GI: disulfide bridges, synthesis, and preparation of iodinated derivatives."

RT Biochemistry 23:2296-2802(1984).

CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they bind to the nicotinic acetylcholine receptors (nAChR) and thus inhibit them.

CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.

CC -!- SIMILARITY: Belongs to the conotoxin A superfamily. Alpha-type family.

DR PIR; A01183; NTXN2G.

DR HSSP; PS5973; 1B45.

KW Postsynaptic neurotoxin; Neurotoxin; Toxin;

KW Acetylcholine receptor inhibitor; Amidation.

FT DISULFID 2 7

FT DISULFID 3 13 AMIDATION.

FT MOD RES 13 13 AMIDATION.

SQ SEQUENCE 13 AA; 1422 MW; DEEEB31C3297EBD CRC64;

Query Match 32.6%; Score 15; DB 1; Length 13;

Best Local Similarity 60.0%; Pred. No. 4.8e+03; Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GSFFS 5

DB 8 GKHF 12

RESULT 14

KARA_BROPL ID KARA_BROPL STANDARD; PRT; 14 AA.

AC P22474; DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Karatasin (EC 3.4.22.-) (Fragment).

OS Bromelia plumieri (Karatas).

OC Bokaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Bromeliaceae;

OC Bromelia.

NCBI_TaxID=4617; [1]

OX RN RP SEQUENCE.

RX MEDLINE=90344224; PubMed=1368518;

RA Montes C., Amador M., Cuevas D., Cordoba F.; RT "Subunit structure of karatasin, the proteinase isolated from Bromelia plumieri (karatas)." Agric. Biol. Chem. 54:17-24 (1990).

RL CC -!- SUBUNIT: Dimer of two small subunits linked by disulfide bonds.

DR DR InterPro: IPR000169; SHPr0t_acsite.

DR PROSITE: PS00139; THIOL_PROTEASE_CYS; PARTIAL.

DR PROSITE; PS00639; THIOL_PROTEASE_HIS; PARTIAL.

DR PROSITE; PS00640; THIOL_PROTEASE ASN; PARTIAL.

DR KW Hydrolase; Thio protease.

FT NON_TER 14 14 SQ SEQUENCE 14 AA; 1602 MW; FDA156893F0834FA CRC64;

Query Match 32.6%; Score 15; DB 1; Length 14;

Best Local Similarity 66.7%; Pred. No. 5.2e+03; Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 ELW 8

DB 3 ETW 5

RESULT 15

CORZ_2PEAM ID CORZ_2PEAM STANDARD; PRT; 11 AA.

AC P1496; DT 01-OCT-1989 (Rel. 12, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Corazonin.

OS Periplaneta americana (American cockroach).

OC Burkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;

OC Blattidae; Periplaneta.

NCBI_TaxID=6978; [1]

RN RP SEQUENCE.

RC TISSUE=Corpora cardiaca;

RX MEDLINE=1932572; PubMed=2753132;

RA Veenstra J.A.; RT "Isolation and structure of corazonin, a cardioactive peptide from the American cockroach,"

RT FEBS Lett. 250:231-234 (1989).

RL CC -!- FUNCTION: Cardioactive Peptide. Corazonin is probably involved in the physiological regulation of the heart beat.

CC -!- SUBCELLULAR LOCATION: Secreted.

DR PIR; S05002; S05002.

KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
MOD RES 1
FT PYRROLIDONE CARBOXYLIC ACID.
MOD PBS 11
FT AMIDATION.
SQ SEQUENCE 11 AA; 1387 MW; C7CFF32D6415AB46 CRC64;
Query Match 30.4%; Score 14; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 6.3e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 FSELW 8
: 5 YSRGW 9
Db

Search completed: September 20, 2004, 17:31:08
Job time : 10 secs

GenCore version 5.1.6
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OM protein - protein search, using sw mode

Run on: September 20, 2004, 17:29:05 ; Search time 15 Seconds
(without alignments)
51.302 Million cell updates/sec

Title: AUDET-SEQ1
Perfect score: 46
Sequence: 1 gsfseew 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:

1421

Minimum DB seq length: 11
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

PIR_78;*
1: PIR1;*
2: PIR2;*
3: PIR3;*
4: PIR4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	50.0	15	2 PH1613	Ig H chain V-D-J r
2	22	47.8	15	2 F29501	Fibronopeptide A -
3	20	43.5	13	2 S32473	LymnaDFamide 3 - g
4	20	43.5	13	2 H56046	urinary trct ston
5	19	41.3	15	2 I29501	fibronopeptide A -
6	19	41.3	15	2 S34956	Ig mu chain V regi
7	18	39.1	11	1 LFTWWE	probable trps lea
8	18	39.1	11	2 S33300	probable subsance
9	18	39.1	14	2 A17150	Glucose 1-dehydrog
10	18	39.1	15	2 PH1366	Ig heavy chain DJ
11	17	37.0	12	2 PH1189	T-cell receptor al
12	17	37.0	12	2 PH1180	T-cell receptor al
13	17	37.0	12	2 PH1183	T-cell receptor al
14	17	37.0	12	2 PH1188	T-cell receptor al
15	17	37.0	12	2 PH1172	T-cell receptor al
16	17	37.0	12	2 PH1175	T-cell receptor al
17	17	37.0	14	2 B44854	L-2,4-diaminobuty
18	17	37.0	14	2 PH1448	T-cell receptor al
19	17	37.0	14	2 PH0945	T-cell receptor al
20	17	37.0	14	2 S26516	T-cell receptor be
21	17	37.0	15	2 S26524	T-cell receptor al
22	17	37.0	15	2 S26527	T-cell receptor al
23	17	37.0	15	2 S26528	T-cell receptor al
24	17	37.0	15	2 S26534	T-cell receptor al
25	17	37.0	15	2 PH1436	T-cell receptor al
26	17	37.0	15	2 PH1365	Ig heavy chain DJ
27	16.5	35.9	15	2 C53652	rhlR Protein -
28	16	34.8	11	2 PT0302	Ig heavy chain CRD
29	16	34.8	11		

30	16	34.8	12	2 I64829	gene HEXA protein
31	16	34.8	12	2 PT0274	Ig heavy chain CRD
32	16	34.8	12	2 PH1324	Ig heavy chain DJ
33	16	34.8	12	2 PH1308	Ig heavy chain DJ
34	16	34.8	12	2 S74144	aggrecan - bovine
35	16	34.8	12	2 PH1467	T-cell receptor be
36	16	34.8	12	2 I41235	Glutamine-tRNA lig
37	16	34.8	13	2 I51905	collecting duct wa
38	16	34.8	12	2 A60822	somatostatin - spo
39	16	34.8	14	2 A58963	alpha-conotoxin Cn
40	16	34.8	14	2 A35105	hypothetical prote
41	16	34.8	14	2 S33931	S-allele-associate
42	16	34.8	15	2 PH1319	Ig heavy chain DJ
43	16	34.8	15	2 PA0110	translation elonga
44	16	34.8	15	2 PR0076	fructose-bisphosph
45	15	32.6	11	2 B49164	chromogranin-B - r

ALIGNMENTS

RESULT 1	PH1613	Ig H chain V-D-J region (clone B-less 17) - mouse (fragment)	Query Match 50.0%; Best Local Similarity 50.0%; Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
	C;Species: Mus musculus (house mouse)	C;Accession: PH1613	
	C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999	R;Levinson, D.A.; Campos-Torres, J.; Leder, P.	
	C;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice	J;Exp. Med. 178, 317-329, 1993	
	A;Reference number: PH1580; PMID:93301609; PMID:8315387	A;Accession: PH1613	
	A;Molecule type: DNA	A;Experimental source: bone marrow pre-B lymphocyte	
	A;Residues: 1-15 <LEV>	C;Keywords: immunoglobulin	
QY	3 FFSEWW 8	Db 9 YFTMW 14	
RESULT 2	F29501	Fibronopeptide A - wombat	Query Match 47.8%; Best Local Similarity 66.7%; Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
	C;Species: Vombatia gen. sp. (wombat)	C;Accession: F295001	
	C;Date: 21-Nov-1997 #sequence_revision 08-Aug-2000 #text_change 18-Aug-2000	R;Blomback, B.; Blomback, M.; Hann, C.	
	C;Unpublished results, cited by Blomback, B., and Blomback, M., in Chemotaxonomy and Se	unpublished results, cited by Blomback, B., and Blomback, M., in Chemotaxonomy and Se	
	A;Reference number: A25501	A;Accession: F29501	
	A;Status: Preliminary	A;Molecule type: protein	
	A;Residues: 1-15 <ELQ>	C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology	
QY	1 GSFESE 6	Db 5 GSFESE 10	
RESULT 3	S32473	lymnaDFamide 3 - great pond snail	Query Match 47.8%; Best Local Similarity 66.7%; Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

C;Species: *Lymnaea stagnalis* (great pond snail)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
C;Accession: S32473
R;Johnsen, A.H.; Rehfeld, J.F.
R;Biochem., 213, 875-879, 1993
A;Title: Lymnaeidae, a new family of neuropeptides from the pond snail, *Lymnaea stagnalis*
A;Reference number: S32471; MUID:93238777; PMID:8477756
A;Accession: S32473
A;Molecule type: protein
A;Residues: 1-13 <OR>
A;Cross-references: PIDN:AAB26364_1; PID:9299831
A;Experimental source: ganglia
C;Keywords: amidated carboxyl end; neuropeptide F;13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 43.5%; Score 20; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GSFFSE 6
Db 7 GSAFSD 12

RESULT 4
H56046 urinary tract stone matrix protein 10, 42K - human (fragment)
C;Species: *Homo sapiens* (man)
C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 12-Apr-1995
C;Accession: H56046
R;Binette, J.P.; Binette, M.B.; Gaviniowicz, M.A.; Kendrick, N.
Submitted to the Protein Sequence Database, February 1995
A;Description: Isolation, characterization and sequence of stone proteins.
A;Reference number: H56046
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <BIN>

Query Match 43.5%; Score 20; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SFESL 7
Db 3 SYFNDL 8

RESULT 5
I29501 fibrinopeptide A - kangaroo
C;Species: *Macropus* sp. (kangaroo)
C;Accession: I29501
R;Blomhaeck, B.; Blomhaeck, M.; Hann, C.
Unpublished results, cited by Blomhaeck, B., and Blomhaeck, M., in Chemotaxonomy and Serological relationships of kangaroos, 1995
A;Reference number: A29501
A;Accession: I29501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <BL0>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 41.3%; Score 19; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GSFFSE 6
Db 5 GTFLAE 10

RESULT 6

S43956 Ig mu chain V region (clone 17) - human (fragment)
C;Species: *Homo sapiens* (man)
C;Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C;Accession: S43956
R;Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.
Nucleic Acids Res. 22, 1389-1393, 1994
A;Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
A;Reference number: S43956; MUID:94248036; PMID:8190629
A;Accession: S43956
A;Molecule type: DNA
A;Residues: 1-15 <AG>
C;Keywords: immunoglobulin

Query Match 41.3%; Score 19; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1 GSFFSELW 8
Db 7 GSF-DWV 12

RESULT 7
LFTWIE probable trpE leader peptide - *Thermus aquaticus*
C;Species: *Thermus aquaticus*
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
C;Accession: S03315
R;Sato, S.; Nakada, Y.; Kanaya, S.; Tanaka, T.
Biochim. Biophys. Acta 950, 303-312, 1988
A;Title: Molecular cloning and nucleotide sequence of *Thermus thermophilus* HB8 trpE and
A;Reference number: S03315; MUID:89000781; PMID:2844259
A;Accession: S03315
A;Molecule type: DNA
A;Residues: 1-11 <SAT>
A;Cross-references: EMBL:X07744; NID:948261; PIDN:CAA30565_1; PID:948262
A;Note: the source is designated as *Thermus thermophilus* HB8
C;Genetics:
A;Gene: trpL
C;Superfamily: probable trpE leader peptide

Query Match 39.1%; Score 18; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 SELW 8
Db 5 SALW 8

RESULT 8
S33300 probable substance P - smaller spotted catshark
C;Species: *Scyliorhinus canicula* (smaller spotted catshark)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Mar-1999
C;Accession: S33300
R;Waugh, D.; Wang, Y.; Hazen, N.; Balment, R.J.; Conlon, J.M.
Bur. J. Biochem. 214, 463-474, 1993
A;Title: Primary structures and biological activities of substance-P-related peptides f
A;Reference number: S33300; MUID:93292308; PMID:7685693
A;Accession: S33300
A;Molecule type: protein
A;Residues: 1-11 <WAU>
A;Experimental source: brain
C;Function:
A;Description: may play a physiological role in the regulation of cardiovascular and ga
A;Note: substance P is derived by post-translational processing of preprotachykinin A
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 39.1%; Score 18; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 1 GSFFSEL 7 Db 6 GGFA~~S~~AL 12

RESULT 9
 A17150 glucose 1-dehydrogenase (NAD) (EC 1.1.1.118) - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 03-Jun-2002
 C;Accession: A17150
 R;Franzen, B.; Carrubba, C.; Feingold, D.S.; Ashcom, J.; Franzen, J.S.
 A;Title: Amino acid sequence of the tryptic peptide containing the catalytic-site thiol
 A;Reference number: A17150; MUID:82182061; PMID:6896145
 A;Molecule type: protein
 A;Residues: 1-14 <WAS>
 C;Keywords: NAD; oxidoreductase

Query Match 39.1%; Score 18; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 2.e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GSFFSE 6
 Db 7 GSCFZZ 12

RESULT 10
 PH1366 Ig heavy chain DJ region (clone C111-106) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C;Accession: PH1366
 R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph
 A;Reference number: PH1302; MUID:93094761; PMID:1460419
 A;Accession: PH1366
 A;Molecule type: DNA
 A;Residues: 1-15 <WAS>
 C;Keywords: heterotetramer; immunoglobulin

Query Match 39.1%; Score 18; DB 2; Length 15;
 Best Local Similarity 16.7%; Pred. No. 3.e+03;
 Matches 1; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Qy 3 FFSEIW 8
 Db 6 YYGDIW 11

RESULT 11
 PH1189 T-cell receptor alpha chain V region (Cw3/Cas11) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C;Accession: PH1189
 R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
 J. Exp. Med. 176, 439-447, 1992
 A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
 A;Reference number: S26512; MUID:92364546; PMID:1380061
 A;Accession: PH1189
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-12 <CAS>

Query Match 37.0%; Score 17; DB 2; Length 12;
 Best Local Similarity 57.1%; Pred. No. 3.7.e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GSFFSPL 7
 |
 |
 |
 Db 6 GGRASAL 12

RESULT 15
 PH1172
 T-cell receptor alpha chain V region (Cw3/Cas15) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C;Accession: PH1172
 R;Catanova, J.I.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
 J. Exp. Med. 176, 439-447, 1992
 A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
 A;Reference number: S26512; PMID:92364546; PMID:1380061
 A;Accession: PH1172
 A;Status: Preliminary
 A;Molecule type: mRNA
 A;Residues: 1-12 <CAS>
 Query Match 37.0%; Score 17; DB 2; Length 12;
 Best Local Similarity 57.1%; Pred. No. 3.7e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 GSFFSPL 7
 |
 |
 |
 Db 6 GGRASAL 12

Search completed: September 20, 2004, 17:32:10
 Job time : 16 secs

	KW	beta-1 adrenergic activated antibody; immunosuppressive.
	XX	
Y	OS	Synthetic.
Db	XX	
	Key	Location/Qualifiers
	Modified-site	14
	FT	/note= "Lys modified with an amide or free acid group"
	XX	
	PN	WO200121660-A1.
	XX	
	PD	29-MAR-2001.
	XX	
	PF	21-SEP-2000; 2000WO-EP009241.
	XX	
	PR	21-SEP-1999; 99EP-00118630.
	PR	21-SEP-1999; 99EP-00118631.
	XX	
	PA	(AFFI-) AFFINA IMMUNTECHNIK GMBH.
	PA	Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
	XX	
	PI	
	XX	
	DR	WPI; 2001-335469/35.
	XX	
	PT	New peptide useful for combating the autoantibodies that are responsible for dilatative cardiomyopathy.
	PT	
	XX	
	PS	Claim 4; Page 22; 29pp; German.
	XX	
	CC	This invention describes a novel peptide (P1) which can be used for (1) isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid phase; and (2) a chromatographic apparatus with (P1) bound. The products of the invention have cardiotropic and immunosuppressive activity. (P1) is used to produce medicine to combat beta-1 adrenergic activated autoantibodies having a causal pathological relationship with dilatative cardiomyopathy. This sequence represents a specifically claimed peptide used to illustrate the method of the invention
	CC	
	CC	Sequence 14 AA;
	CC	Query Match 100.0%; Score 55; DB 4; Length 14;
	CC	Best Local Similarity 100.0%; Pred. No. 0.0047; Mismatches 0; Indels 0; Gaps 0;
	CC	Matches 10; Conservative 0; Gaps 0; Indels 0; Gaps 0;
	QY	1 GSFFSELWTS 10
	DB	2 GSFFSELWTS 11
	XX	
	RESULT 4	
	ID	AAB86020 standard; peptide; 14 AA.
	XX	
	AC	AAB86020;
	XX	
	AC	29-JUL-2001 (first entry)
	XX	
	DB	DCM autoantibody-associated peptide #1.
	XX	
	KW	DCM; dilatative cardiomyopathy; beta-1-adrenergic receptor; cardiotropic antibody; myocardial.
	XX	
	OS	Synthetic.
	XX	
	Key	Location/Qualifiers
	Modified-site	1
	FT	/note= "N-terminal acetylated"
	FT	14
	FT	/note= "C-terminal amide"
	XX	
	PN	D1E19945211-A1.
	XX	
	PD	29-MAR-2001.
	XX	
RESULT 2	3	
Y	ID	AAB86012 standard; peptide; 14 AA.
Db	XX	
	AC	AAB86012;
	XX	
	AC	12-JUL-2001 (first entry)
	XX	
	DE	DCM-associated peptide #12.
	XX	
	DCM; dilatative cardiomyopathy; autoantibody; cardiotropic antibody; myocardial.	

PF 21-SEP-1999; 99DE-01045211.
 XX
 PR 21-SEP-1999; 99DE-01045211.
 XX
 PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.
 XX
 Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
 PI DR: 2001-301259/32.
 XX
 New autoantibody-binding peptides with an amino acid sequence
 PT corresponding a beta-1-adrenergic receptor group useful for treating
 PT dilatative cardiomyopathy.
 XX
 PS Claim 2; Page 5; 8pp; German.

XX This invention describes novel peptides (I) with an amino acid sequence corresponding a beta-1-adrenergic receptor group recognized by autoantibodies associated with dilatative cardiomyopathy (DCM). The invention also describes a chromatographic device comprising (I) bound to a solid phase. The products of the invention have cardiant activity. (I) are useful for treating DCM by binding autoantibodies directed against myocardial beta-1-adrenergic receptors, either by neutralizing the antibodies in vivo or by extracorporeal treatment of blood or plasma with (I) immobilized on a solid phase. This sequence represents a specifically claimed peptide used to illustrate the method of the invention.

XX Sequence 14 AA;

Query Match 100.0%; Score 55; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.0047;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSFFSELWTS 10
 Db 2 GSFFSELWTS 11

RESULT 5
 ID AAB86013 standard; Peptide; 15 AA.
 XX
 AC AAB86013;
 XX DT 12-JUL-2001 (first entry)
 DE DCM-associated peptide #3.
 KW DCM; dilatative cardiomyopathy; autoantibody; cardiant;
 KW beta-1 adrenergic activated antibody; immunosuppressive.
 XX Synthetic.
 XX Key Location/Qualifiers
 FT 15 /note= "Lys modified with an amide or free acid group"
 FT
 XX PN WO200121660-A1.
 PR 21-SEP-1999; 99EP-00119630.
 XX
 PD 29-MAR-2001.
 XX
 PP 21-SEP-2000; 2000WO-EP009241.
 XX PR 21-SEP-1999; 99EP-00119631.
 XX
 PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.
 XX
 PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
 DR DR: 2001-335469/35.
 XX
 PT New peptide useful for combatting the autoantibodies that are responsible

PT for dilatative cardiomyopathy.
 XX
 PS Claim 4; Page 22; 29pp; German.

XX This invention describes a novel peptide (P1) which can be used for (1) isolating beta-1-adrenergic activated antibodies bound to (P1) on a solid phase; and (2) a chromatographic apparatus with (P1) bound. The products of the invention have cardiant and immunosuppressive activity. (P1) is used to produce medicine to combat beta-1 adrenergic activated autoantibodies having a causal pathobological relationship with dilatative cardiomyopathy. This sequence represents a specifically claimed peptide used to illustrate the method of the invention.

XX Sequence 15 AA;

Query Match 100.0%; Score 55; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0051;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSFFSELWTS 10
 Db 3 GSFFSELWTS 12

RESULT 6
 ID AAB86021 standard; peptide; 15 AA.
 XX
 AC AAB86021;
 XX DT 12-JUL-2001 (first entry)
 DE DCM autoantibody-associated peptide #2.
 KW DCM; dilatative cardiomyopathy; beta-1-adrenergic receptor; cardiant;
 KW autoantibody; myocardial.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetylated"
 FT Modified-site 15 /note= "C-terminal amide"
 FT
 XX DE19945211-A1.
 PR 21-SEP-1999; 99DE-01045211.
 XX
 PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.
 XX
 PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
 DR WPI; 2001-301259/32.
 XX
 PT New autoantibody-binding peptides with an amino acid sequence corresponding a beta-1-adrenergic receptor group useful for treating dilatative cardiomyopathy.

XX
 PS Claim 2; Page 5; 8pp; German.

XX This invention describes novel peptides (I) with an amino acid sequence corresponding a beta-1-adrenergic receptor group recognized by autoantibodies associated with dilatative cardiomyopathy (DCM). The invention also describes a chromatographic device comprising (I) bound to a solid phase. The products of the invention have cardiant activity. (I) are useful for treating DCM by binding autoantibodies directed against myocardial beta-1-adrenergic receptors, either by neutralizing the antibodies in vivo or by extracorporeal treatment of blood or plasma with

CC	(1) immobilized on a solid phase. This sequence represents a specifically claimed peptide used to illustrate the method of the invention.
CC	Sequence 15 AA;
SQ	Query Match 100.0%; Score 55; DB 4; Length 15; Best Local Similarity 100.0%; Pred. No. 0.005%; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	1 GSFFEBELWTS 10 DB 3 GSFFEBELWTS 12
XX	RESULT 7
AA09130	AA09130 standard; protein; 8 AA.
ID	AA09130;
XX	AC AA09130;
DT	06-AUG-2003 (revised) 30-AUG-2000 (first entry)
XX	DE Hepatitis GB virus protein sequence SEQ ID NO:252.
XX	KW Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic; infection;
KW	detection; characterisation; hepatitis.
XX	Hepatitis GB virus.
OS	XX
XX	US6051374-A.
PN	XX
XX	PD 18-APR-2000.
XX	PF 07-JUN-1995; 95US-00488445.
XX	PR 14-FEB-1994; 94US-00196030.
PR	13-MAY-1994; 94US-00242654.
PR	29-JUL-1994; 94US-00283314.
PR	23-NOV-1994; 94US-00344185.
PR	23-NOV-1994; 94US-00344190.
PR	30-JAN-1995; 95US-00377557.
XX	(ABBO) ABBOTT LAB.
PA	XX Dawson GU, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buijk SL;
PI	Mushahwar IK, Simons JN, Desai SM, Ecker JC, Schlauder GG;
XX	WPI: 2000-338307/29.
XX	Detecting target hepatitis GB virus nucleic acid in a test sample suspected of containing HGBV comprises reacting the test sample the HGBV polynucleotide probe and detecting the complex that contains target HGBV.
XX	Example 9; Col 331-332; 369pp; English.
XX	The present invention describe a method for detecting target hepatitis GB virus (HGBV) nucleic acid (THN) in a test sample (T) suspected of containing HGBV. The method involves reacting (T) with a HGBV polynucleotide probe (I) containing 15 contiguous nucleotides, and which selectively hybridizes to the HGBV genome or its full complement, and detecting the complex that contains THN, indicating the presence of target HGBV. The method is used for detecting target HGBV nucleic acid in the test sample suspected of containing HGBV and for characterisation of newly ascertained etiological agent of non-A, non-B, non-C, non-D and non-E hepatitis causing collectively as hepatitis GB virus. AA05270 to AA55489 and AA08985 to AA08480 represent nucleotide and protein sequences used in the exemplification of the present invention. (Updated on 06-AUG-2003 to correct OS field.)
XX	Sequence 8 AA;
SQ	Query Match 61.8%; Score 34; DB 3; Length 8;

SQ	Sequence 18 AA;	CC	preservative to increase or decrease storage capabilities.
	Query Match 61.8%; Score 34; DB 5; Length 18;	CC	AAU91148 represent human secreted protein sequences
	Best Local Similarity 85.7%; Fred. No. 34;	XX	
	Matches 6; Conservative 0; Mismatches 1; Indels 0;	SQ	Sequence 18 AA;
Qy	4 FSELWTS 10	Query Match 61.8%;	Score 34; DB 5; Length 18;
		Best Local Similarity 85.7%;	Pred. No. 34;
Ds	3 FSEAWNTS 9	Matches 6; Conservative 0;	Mismatches 1; Indels 0;
		Oy	Gaps 0;
		Db	
RESULT 9		4 FSELWTS 10	
AAU91081			
ID	AAU91081 standard; protein; 18 AA.	3 FSEAWNTS 9	
XX			
AC	ABG65209		
XX	ID ABG65209 standard; protein; 18 AA.		
DT	05-JUN-2002 (first entry)		
XX			
DE	Human secreted protein sequence #1.		
XX			
KW	Human secreted protein; autoimmune disease; hyperproliferative disorder;		
KW	cardiovascular disorder; cerebrovascular disorder; infection; cancer;		
KW	nervous system disorder; ocular disorder; epithelial cell proliferation;		
KW	wound healing; skin ging; sunburn; transplantation; chemotaxis;		
KW	tissue regeneration; food additive; preservative; cytostatic; cardiant;		
KW	KW antiviral; antiallergic; antiinflammatory; antibacterial; antifungal.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200218412-A1.		
XX			
PD	07-MAR-2002.		
XX			
PP	17-JAN-2001; 2001WO-US001384.		
XX			
PR	28-AUG-2000; 2000US-0228086P.		
PR	04-JAN-2001; 2001US-0259516P.		
XX			
PA	(HUMA-) HUMAN GENOME SCI INC.		
XX			
PI	Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR;		
PI	Olsen HS, Moore PA, Wei P, Ebner R, Duan RD, Shi Y, Choi GH;		
PI	Fiscella M, Ni J;		
XX			
DR	WPI: 2002-269525/31.		
DR	N-PSDB; ABG54119.		
XX			
PT	Seventeen nucleic acid molecules encoding human secreted proteins, useful		
PT	in the prevention, treatment and diagnosis of cancer, immune disorders,		
PT	cardiovascular disorders and neurological diseases.		
XX			
PS	Claim 11; Page 450; 505pp; English.		
XX			
CC	The present invention relates to the isolation of novel human secreted		
CC	proteins, and the polynucleotide sequences encoding them. The secreted		
CC	proteins are useful to prevent, treat or ameliorate a medical condition		
CC	in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or		
CC	sheep. The secreted proteins are also useful in diagnosing a pathological		
CC	condition or susceptibility to a pathological condition. Antibodies to		
CC	the secreted proteins can also be used in alleviating symptoms associated		
CC	with disorders and in diagnostic immunoassays e.g. radioimmunoassays or		
CC	enzyme linked immunosorbent assays (ELISA). Disorders which can be		
CC	diagnosed or treated include autoimmune diseases e.g. rheumatoid		
CC	arthritis, hyperproliferative disorders e.g. cancer, cardiovascular		
CC	disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral		
CC	ischaemia, angiogenesis, nervous system disorders e.g. Parkinson's		
CC	disease, infections caused by bacteria, viruses and fungi and ocular		
CC	disorders e.g. cornual infection. The polypeptides can also be used to		
CC	aid wound healing and epithelial cell proliferation, to prevent skin		
CC	aging due to sunburn, to maintain organs before transplantation, for		
CC	supporting cell culture of primary tissues, to regenerate tissues and in		
CC	chemotaxis. The polypeptides can also be used as a food additive or		
XX			
PS	Claim 1; Page 18; 2102pp; English.		
XX			
CC	The present invention relates to albumin fusion proteins comprising a		
CC	therapeutic protein X and human albumin (HA, also known as human serum		
CC	albumin, HSA). The proteins are useful for treating a disease or disorder		
CC	that may be modulated by therapeutic protein X. The albumin extends the		
CC	shelf-life of protein X, and may increase its biological in vitro/in vivo		
CC	activity. The protein is useful for treating and diagnosing disorders		
CC	such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's		
CC	disease, ulcerative colitis), immune disorders (e.g. acquired		
CC	immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),		
CC	haematoopoietic disorders, neural disorders (e.g. Alzheimer's,		
CC	schizophrenia, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,		
CC	schizophrenic, and connective disorders (e.g. osteoporosis, arthritis).		
CC	ABG63326-ABG6518 represent albumin fusion proteins of the invention		
XX			
SQ	Sequence 18 AA;	SQ	Sequence 18 AA;

Query Match	61.8%	Score 34;	DB 5;	Length 18;				
Best Local Similarity	85.7%;	Pred. No. 34;						
Matches	6;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps 0;
QY	4 FSELWTS 10							
Db	3 FSEAWTS 9							
RESULT 1.1								
ABG65210	ABG65210 standard; protein; 18 AA.							
ID	ABG65210							
XX	DT -AUG-2002 (first entry)							
XX	Human albumin fusion protein #1885.							
XX	Albumin fusion protein; therapeutic protein X; human albumin; HA; human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiflammatory; antilulcer; immunomodulator; anti-HIV; antidiabetic; haemototic; nootropic; neuroprotective; antiparkinsonian; antimicrobial; neuroleptic; osteopathic; antiarthritic.							
XX	Homo sapiens.							
OS	Synthetic.							
XX	WO2001171137-A1.							
XX	18-OCT-2001.							
PD	PT 12-APR-2001; 2001WO-US011988.							
XX	12-APR-2000; 2000US-0229358P.							
PR	25-APR-2000; 2000US-0129384P.							
PR	21-DEC-2000; 2000US-0256931P.							
PA	(HUMA-) HUMAN GENOME SCI INC.							
XX	Rosen CA, Haseltine WA;							
PI	WI; 2002-010886/01.							
PT	New fusion protein for treating disease e.g. diabetes comprises an albumin fused to a therapeutic protein.							
XX	Claim 1; Page 1828; 2102PP; English.							
PS	XX							
The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA), also known as human serum albumin, (HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).								
CC	ABG63326 ABG55518 represent albumin fusion proteins of the invention.							
XX	Sequence 18 AA;							
Query Match	61.8%	Score 34;	DB 5;	Length 18;				
Best Local Similarity	85.7%;	Pred. No. 34;						
Matches	6;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps 0;
QY	4 FSELWTS 10							
Query Match	61.8%	Score 34;	DB 5;	Length 18;				
Best Local Similarity	85.7%;	Pred. No. 34;						
Matches	6;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps 0;

XX Key Location/Qualifiers
PT Modified-site 15
FT /note= "Lys modified with an amide or free acid group"
XX
PN WO200121660-A1.
XX PD 29-MAR-2001.
XX PF 21-SEP-2000; 2000WO-EPO09241.
XX PR 21-SEP-1999; 99EP-00118630.
XX PR 21-SEP-1999; 99EP-00118631.
XX PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.
XX PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
XX DR WPI; 2001-3-01259/32.
XX PD New antibody-binding peptides with an amino acid sequence
PT corresponding a betal-adrenergic receptor group useful for treating
PT dilatative cardiomyopathy.
XX
PS Claim 2; Page 5; 8pp; German.
XX
CC This invention describes novel peptides (I) with an amino acid sequence
CC corresponding a beta-1-adrenergic receptor group recognized by
CC autoantibodies associated with dilatative cardiomyopathy (DCM). The
CC invention also describes a chromatographic device comprising (I) bound to
CC a solid phase. The products of the invention have cardiot activity. (I)
CC are useful for treating DCM by binding autoantibodies directed against
CC myocardial beta-1-adrenergic receptors, either by neutralizing the
CC antibodies in vivo or by extracorporeal treatment of blood or plasma with
CC (I) immobilized on a solid phase. This sequence represents a specifically
CC claimed peptide used to illustrate the method of the invention
XX
SQ Sequence 15 AA;
Query Match 60.0%; Score 33; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 42;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
CC
Qy 1 GSFFSEIWTS 10
Db 3 GTLFSDFWLS 12
XX
RESULT 15
AA020307
ID AAO20307 standard; peptide; 15 AA.
XX
AC AAO20307;
XX DT 31-MAY-2002 (first entry)
XX DB Human plectin 10 protein N-terminal region.
XX KW Human plectin 10; DNA recombination; cancer; HIV infection.
XX OS Homo sapiens.
XX PN CN1325901-A.
XX PD 12-DEC-2001.
XX DE DCM autoantibody-associated peptide #3.
XX KW DCM; dilatative cardiomyopathy; beta-1-adrenergic receptor; cardiot;
KW autoantibody; myocardial.
XX
OS Synthetic.
XX
Key Location/Qualifiers
PT Modified-site 1
FT /note= "N-terminal acetylated"
FT 15
FT /note= "C-terminal amide"
PN DE19945211-A1.
XX PD 29-MAR-2001.
XX PF 21-SEP-1999; 99DE-01045211.
XX PR 21-SEP-1999; 99DE-01045211.
XX
PS Example 5; Page 18 (Disclosure); 33pp; Chinese.
XX
PT Polypeptide-human plectin 10 and polynucleotide encoding it.
XX
PS WPI; 2002-196661/26.
XX
PS Example 5; Page 18 (Disclosure); 33pp; Chinese.
XX
CC The invention relates to the novel polypeptide-human plectin 10, the
CC polynucleotide encoding it, the process for preparing the polypeptide by
CC DNA recombination, the application of the polypeptide in treating
CC diseases such as cancer and HIV infection. The invention also relates to
CC the antagonist of the polypeptide and its medical action, and the
CC application of the polynucleotide. This sequence represents an N-terminal

CC region of the human plectin 10 protein of the invention
XX

SQ Sequence 15 AA:

Query Match 60.0%; Score 33; DB 5; Length 15;
Best Local Similarity 55.6%; Pred. No. 42;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SFFEBELWTS 10
 :|||: :|
Db 2 AFFSSIWLS 10

Search completed: August 27, 2004, 09:25:43
Job time : 127 secs

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OM protein - protein search, using sw model

Run on: August 27, 2004, 09:22:53 ; Search time 31 Seconds
(without alignments)

16.654 Million cell updates/sec

Title: AUDET681-1
Perfect score: 55
Sequence: 1 gffffselwts 10

Scoring table: BLOSUM62
Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 186303

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
 1: /cgnd_6/prodata/2/iaa/5A_COMB.pep:
 2: /cgnd_6/prodata/2/iaa/5B_COMB.pep:
 3: /cgnd_6/prodata/2/iaa/6A_COMB.pep:
 4: /cgnd_6/prodata/2/iaa/6B_COMB.pep:
 5: /cgnd_6/prodata/2/iaa/PC10S_COMB.pep:
 6: /cgnd_6/prodata/2/iaa/backfile1.pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB ID	Description
1	34	61.8	8	4	US-08-469-260A-252	Sequence 252, App
2	34	61.8	8	4	US-08-488-446-252	Sequence 252, App
3	34	61.8	8	4	US-08-467-344-252	Sequence 252, App
4	31	56.4	18	2	US-08-934-935-125	Sequence 125, App
5	30	54.5	6	1	US-08-124-957-6	Sequence 6, Appli
6	30	54.5	6	3	US-09-035-666-6	Sequence 6, Appli
7	30	54.5	11	1	US-08-424-957-42	Sequence 6, Appli
8	30	54.5	11	3	US-09-035-666-42	Sequence 42, Appli
9	30	54.5	19	4	US-09-081-955-13	Sequence 13, Appli
10	28	50.9	11	3	US-09-186-958-6	Sequence 6, Appli
11	28	50.9	11	3	US-09-659-21A-6	Sequence 6, Appli
12	28	50.9	11	4	US-09-081-276-6	Sequence 6, Appli
13	28	50.9	13	2	US-08-537-79B-388	Sequence 388, App
14	28	50.9	13	3	US-08-871-35A-388	Sequence 388, App
15	28	50.9	13	4	US-09-201-57-388	Sequence 2, Appli
16	27	49.1	6	1	US-08-277-660A-2	Sequence 2, Appli
17	27	49.1	6	1	US-08-124-957-2	Sequence 2, Appli
18	27	49.1	6	3	US-09-035-666-2	Sequence 2, Appli
19	27	49.1	6	4	US-09-081-975-1	Sequence 1, Appli
20	27	49.1	6	4	US-09-128-02B-130	Sequence 130, App
21	27	49.1	7	1	US-08-277-660A-27	Sequence 27, Appli
22	27	49.1	7	1	US-08-424-957-15	Sequence 19, Appli
23	27	49.1	7	1	US-08-124-957-19	Sequence 19, Appli
24	27	49.1	7	3	US-09-035-666-15	Sequence 15, Appli
25	27	49.1	7	3	US-09-035-666-19	Sequence 15, Appli
26	27	49.1	10	1	US-08-277-660A-7	Sequence 7, Appli
27	49.1	10	1	US-08-424-957-11	Sequence 11, Appli	

ALIGNMENTS

RESULT 1
US-08-469-260A-252
; Sequence 252, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAM J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SUBRESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHEIKI L. BUIK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3100
; COMPUTER READABLE FORM:
; COMPUTER TYPE: Floppy diskible
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469, 260A
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/424, 550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-938-2623
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acids
; MOLECULE TYPE: linear
; MOLECULE TYPE: protein

US-08-469-260A-252

RESULT 2

Query Match Score 34; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0

Qy	4 FSEIWTs 10	Score 34; DB 4; Length 8; Best Local Similarity 85.7%; Pred. No. 3e+05; Matches 6; Conservative 0; Mismatches 1; Indels 0
Db	1 FSHLWTS 7	

US-08-488-446-252

; Sequence Application US/08488446

; Patent No. 6558698

; GENERAL INFORMATION:

; APPLICANT: JOHN N. SIMONS

; APPLICANT: TAMI J. PILOT-MATIAS

; APPLICANT: GEORGE J. DAWSON

; APPLICANT: GEORGE G. SCHLAUDER

; APPLICANT: SURESH M. DESAI

; APPLICANT: THOMAS P. LEARY

; APPLICANT: ANTHONY SCOTT MUEHRHOFF

; APPLICANT: JAMES C. ERICK

; APPLICANT: SHERI L. BUIJK

; APPLICANT: ISA K. MUSHAHWAR

; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS

; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE

; NUMBER OF SEQUENCES: 716

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D

; STREET: 100 ABBOTT PARK ROAD

; CITY: ABBOTT PARK

; STATE: IL

; COUNTRY: USA

; ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,446

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/424,550

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: POREMBSKI, PRISCILLA E.

REGISTRATION NUMBER: 33,207

REFERENCE/DOCKET NUMBER: 5527.PC.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 708-937-6365

TELEFAX: 708-938-2623

INFORMATION FOR SEQ ID NO: 252:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-488-446-252

Query Match Score 34; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0

Qy	4 FSEIWTs 10	Score 34; DB 4; Length 8; Best Local Similarity 85.7%; Pred. No. 3e+05; Matches 6; Conservative 0; Mismatches 1; Indels 0
Db	1 FSHLWTS 7	

RESULT 3

US-08-467-344A-252 Sequence 252, Application US/08467344A
 Patent No. 6516568 ; Sequence 125, Application US/08934915
 GENERAL INFORMATION:
 APPLICANT: JOHN N. SIMONS
 TAMI J. PILDT-MATIAS
 GEORGE J. DAWSON
 GEORGE G. SCHLAUDER
 SURESH M. DESAI
 THOMAS P. LEARY
 ANTHONY SCOTT MUERHOFF
 JAMES C. ERKER
 SHERI L. BUIJK
 ISA K. MUSHARWAR
 TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
 NUMBER OF SEQUENCES: 7116
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ABBOTT LABORATORIES
 STREET: 100 ABBOTT PARK ROAD
 CITY: ABBOTT PARK
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,344A
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/424,550
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: POREMBSKI, PRISCILLA E.
 REGISTRATION NUMBER: 33,207
 REFERENCE/DOCKET NUMBER: 5527.PC.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-6365
 TELEFAX: 708-938-75623
 INFORMATION FOR SEQ ID NO: 252:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 252:
 US-08-467-344A-252

Query Match 61.8%; Score 34; DB 4; Length 8;
 Best Local Similarity 87.7%; Pred. No. 3e+05; 0; Gains
 Matches 6; Conservative 0; Mismatches 1; Deletes 0;
 Db 1 FSHLWTS 7

RESULT 4
 US-08-914-915-125
 Sequence 125, Application US/08934915
 GENERAL INFORMATION:
 APPLICANT: DILLNER, JOAKIM
 PATENT NO. 5932412
 APPLICANT: CHENG, HWEE MING
 TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
 TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
 TITLE OF INVENTION: PAPILLOMAVIRUS 1, 11, 16, 18, 31, 33 AND 56,
 TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR

TITLE OF INVENTION: DIAGNOSTIC PURPOSES
 NUMBER OF SEQUENCES: 193
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MASON & ASSOCIATES, P.A.
 STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
 CITY: CLEARWATER
 STATE: FLORIDA
 COUNTRY: U.S.A.
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 3.0
 SOFTWARE: Microsoft Word 6.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/934,915
 FILING DATE: 22-SEP-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/949, 836
 ATTORNEY/AGENT INFORMATION:
 NAME: LOUISE A. Foutch
 REGISTRATION NUMBER: 37,133
 REFERENCE/DOCKET NUMBER: 1946.6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 813-538-3800
 TELEFAX: 813-538-3820
 TELEX:
 INFORMATION FOR SEQ ID NO: 125:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 amino acids
 TYPE: amino acid
 TOPOLogy: linear
 MOLECULE TYPE: peptide
 US-08-934-915-125

Query Match 56.4%; Score 31; DB 2; Length 18;
 Best Local Similarity 62.5%; Pred. No. 36;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SFPSELNT 9
 Db 5 SFPSRTWS 12

RESULT 5
 US-08-424-957-6
 Sequence 6, Application US/08424957
 Patent No. 5703377
 GENERAL INFORMATION:
 APPLICANT: Picklesley, Steven M.
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: Lane, David P.
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESS: Fiehr, Honbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 ZIP: 94111-4187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/124,957
 FILING DATE: 19-APR-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/424,957
 FILING DATE: 19-APR-1995
 APPLICATION NUMBER: US 08/277,660
 FILING DATE: 20-JUL-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Walter H.
 REGISTRATION NUMBER: 24,190
 REFERENCE/DOCKET NUMBER: A-61228/WHD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 TELEX: 910 277299
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown

RESULT 6
 US-09-035-686-6
 Sequence 6, Application US/09035686
 Patent No. 6153391
 GENERAL INFORMATION:
 APPLICANT: Lane, David P.
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: Picklesley, Steven M.
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 NUMBER OF INVENTIONS: Protein and Therapeutic Application Thereof
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESS: Fiehr, Honbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 ZIP: 94111-4187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/035,686
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Walter H.
 REGISTRATION NUMBER: 24,190
 REFERENCE/DOCKET NUMBER: A-61228/WHD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 TELEX: 910 277299
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown

US-09-035-686-6

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; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 60/046,207
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30,628
; REFERENCE/DOCKET NUMBER: 47400
; TELEPHONE: 617-345-6054
; TELEFAX: 617-345-1300
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-081-975-13

Query Match
Best Local Similarity 100.0%; Pred. No 57; Score 30; DB 4; Length 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
US-09-186-958-6
; Sequence 6, Application US/09186958B
; GENERAL INFORMATION:
; APPLICANT: Wheilhan, E. Fayette
; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
; FILE REFERENCE: Dyax-009 0 US sequence listing
; CURRENT APPLICATION NUMBER: US/09/186,958B
; CURRENT FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19
; OTHER INFORMATION: binding polypeptide
; US-09-186-958-6

Query Match
Best Local Similarity 62.5%; Pred. No 74; Score 28; DB 3; Length 11;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 11
US-09-669-271A-6
; Sequence 6, Application US/09669271A
; GENERAL INFORMATION:
; APPLICANT: Wheilhan, E. Fayette
; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
; FILE REFERENCE: Dyax-009 0 US sequence listing
; CURRENT APPLICATION NUMBER: US/09/669,271A
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/186,958
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6

Query Match
Best Local Similarity 62.5%; Pred. No 74; Score 28; DB 3; Length 11;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 12
US-09-881-276-6
; Sequence 6, Application US/09881276
; GENERAL INFORMATION:
; APPLICANT: Wheilhan, E. Fayette
; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
; FILE REFERENCE: Dyx-009 0 US-2
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/669,271
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/186,958
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polypeptide
; US-09-881-276-6

Query Match
Best Local Similarity 62.5%; Pred. No 74; Score 28; DB 4; Length 11;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 13
US-08-637-759B-38B
; Sequence 38B, Application US/08637759B
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; PATENT NO. 5,876,931
; ADDRESS:
; STREET: 2800 One Atlantic Center
; CITY: Atlanta, Georgia
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,759B
; SEQ ID NO 6

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; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31.284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 388:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-637-759B-388

Query Match 50.9%; Score 28; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 88;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

; RESULT 14
US-08-871-355A-388
; Sequence 388, Application US/08871355A
; Patent No. 6018669
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/201,945
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/637,759
; CLASIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31.284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 388:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-09-201-945-388

Query Match 50.9%; Score 28; DB 4; Length 13;
Best Local Similarity 50.0%; Pred. No. 88;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

; RESULT 15
US-09-201-945-388
; Sequence 388, Application US/09201945
; Patent No. 6342215
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/201,945
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/637,759
; CLASIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31.284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 388:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-09-201-945-388

Query Match 50.9%; Score 28; DB 4; Length 13;
Best Local Similarity 50.0%; Pred. No. 88;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

; Search completed: August 27, 2004, 09:28:43
; Job time : 32 secs

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OM protein - protein search, using sw model

Run on: August 27, 2004, 09:26:14 ; Search time 684 Seconds
(without alignments)

4.600 Million cell updates/sec

Title: AUDET681-1

Perfect score: 55

Sequence: 1 gsfselwts 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen Parameters: 268144

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : Published Applications AA:
 1: /cgnd_6/_prodata/2/_pubpaas/_us07_PUBCCOMB.pep:
 2: /cgnd_6/_prodatal/2/_pubpaas/_pct_new_pub.pep:
 3: /cgnd_6/_ptodata/2/_pubpaas/_us06_PUBCOMB.pep:
 4: /cgnd_6/_prodatal/2/_pubpaas/_us06_PUBCOMB.pep:
 5: /cgnd_6/_ptodata/2/_pubpaas/_us07_PUBCOMB.pep:
 6: /cgnd_6/_prodatal/2/_pubpaas/_us07_PUBCOMB.pep:
 7: /cgnd_6/_prodatal/2/_pubpaas/_us08_new_pub.pep:
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 18: /cgnd_6/_prodatal/2/_pubpaas/_us60_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1

US-08-424-550B-252

i Sequence 252, Application US/08424550B

i General Information: Publication No. US2002119447A1

i APPLICANT: JOHN N. SIMONS

i APPLICANT: TAMI J. PILOT-MATIAS

i APPLICANT: GEORGE J. DAWSON

i APPLICANT: GEORGE G. SCHLAUDER

i APPLICANT: SUBESH M. DESAI

i APPLICANT: THOMAS P. LEARY

i APPLICANT: ANTHONY SCOTT MUERHOFF

i APPLICANT: JAMES C. ERICK

i APPLICANT: SHERI L. BUIJK

i APPLICANT: ISA K. MUSHAHWAR

i TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS

i TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE

i NUMBER OF SEQUENCES: 716

i CORRESPONDENCE ADDRESS:

i ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
i STREET: 100 ABBOTT PARK ROAD
i CITY: ABBOTT PARK
i STATE: IL
i COUNTRY: USA
i ZIP: 60064-3500
i COMPUTER READABLE FORM:
i MEDIUM TYPE: Floppy disk
i COMPUTER: IBM PC compatible
i OPERATING SYSTEM: PC-DOS/MS-DOS
i SOFTWARE: Patient Release #1.0, Version #1.25
i CURRENT APPLICATION DATA:
i APPLICATION NUMBER: US/08/424550B
i FILING DATE:
i CLASSIFICATION: 435435
i ATTORNEY/AGENT INFORMATION:
i NAME: PORENSKI, PRISCILLA E.
i REGISTRATION NUMBER: 133,207
i REFERENCE/DOCKET NUMBER: 5527.PC.01

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	61.8	8	US-08-424-550B-252	Sequence 252, App
2	34	61.8	18	US-09-833-245-1958	Sequence 1958, App
3	34	61.8	18	US-09-833-245-1959	Sequence 1959, App
4	30	54.5	10	US-09-214-311-35	Sequence 35, App
5	30	54.5	10	US-09-214-311-36	Sequence 36, App
6	30	54.5	13	US-10-221-042-1	Sequence 1, App
7	30	54.5	19	US-10-155-059-13	Sequence 53, App
8	30	54.5	21	US-10-651-563-53	Sequence 35636, App
9	30	54.5	22	US-09-864-761-3593	Sequence 46, App
10	29	52.7	15	US-10-192-381-46	Sequence 36, App
11	29	52.7	14	US-10-224-356-36	Sequence 17, App
12	29	52.7	18	US-10-224-356-36	Sequence 519, App
13	29	52.7	21	US-10-372-676-519	Sequence 519, App
14	29	52.7	21	US-10-097-065-519	Sequence 35, App
15	28	50.9	9	US-09-486-734A-35	

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-6365
 INFORMATION FOR SEQ ID NO: 252:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-424-550B-252

Query Match 61.8%; Score 34; DB 8; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.2e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 FSELWTS 10
 Db 1 FSHLWTS 7

RESULT 2
 US-09-B3-245-1958
 Sequence 1958, Application US/09833245
 Publication No. US20040010134A1
 GENERAL INFORMATION:
 APPLICANT: Human Genome Sciences, Inc.
 TITLE OF INVENTION: Albumin Fusion Proteins
 FILE REFERENCE: PF546PCT
 CURRENT APPLICATION NUMBER: US/09/833,245
 CURRENT FILING DATE: 2001-04-12
 PRIOR APPLICATION NUMBER: 60/129, 358
 PRIOR FILING DATE: 2000-04-12
 PRIOR APPLICATION NUMBER: 60/256, 931
 PRIOR FILING DATE: 2000-12-21
 PRIOR APPLICATION NUMBER: 60/199, 384
 PRIOR FILING DATE: 2000-04-25
 NUMBER OF SEQ ID NOS: 2267
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NC: 1958
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-833-245-1958

Query Match 61.8%; Score 34; DB 11; Length 18;
 Best Local Similarity 85.7%; Pred. No. 42;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 FSELWTS 10
 Db 3 FSEAWTS 9

RESULT 3
 US-09-833-245-1959
 Sequence 1959, Application US/09833245
 Publication No. US20040010134A1
 GENERAL INFORMATION:
 APPLICANT: Human Genome Sciences, Inc.
 TITLE OF INVENTION: Albumin Fusion Proteins
 FILE REFERENCE: PF546PCT
 CURRENT APPLICATION NUMBER: US/09/833,245
 CURRENT FILING DATE: 2001-04-12
 PRIOR APPLICATION NUMBER: 60/229, 358
 PRIOR FILING DATE: 2000-04-12
 PRIOR APPLICATION NUMBER: 60/256, 931
 PRIOR FILING DATE: 2000-12-21
 PRIOR APPLICATION NUMBER: 60/199, 384
 PRIOR FILING DATE: 2000-04-25
 NUMBER OF SEQ ID NOS: 2267
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NC: 1959
 LENGTH: 18

Query Match 61.8%; Score 34; DB 11; Length 18;
 Best Local Similarity 85.7%; Pred. No. 42;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 FSELWTS 10
 Db 3 FSEAWTS 9

RESULT 4
 US-09-214-371-35
 Sequence 35, Application US/09214371B
 Patent No. US2001001851A1
 GENERAL INFORMATION:
 APPLICANT: Lane, David
 APPLICANT: Bottger, Volker
 APPLICANT: Garcia-Echeverria, Carlos
 APPLICANT: Pickley, Stephen
 APPLICANT: Chene, Patrick
 APPLICANT: Hochkeppel, Heinz-Kurt
 APPLICANT: Garcia-Echeverria, Carlos
 TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
 FILE REFERENCE: 4-20937A/PCT
 CURRENT APPLICATION NUMBER: US/09/214,371B
 CURRENT FILING DATE: 1999-03-26
 PRIOR APPLICATION NUMBER: PCT/EP97/03549
 PRIOR FILING DATE: 1997-07-04
 NUMBER OF SEQ ID NOS: 83
 SEQ ID NO: 35
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: peptide
 NAME/KEY: VARIANT
 LOCATION: (1)
 OTHER INFORMATION: X = Ac-Cys(Acrd)
 NAME/KEY: VARIANT
 LOCATION: (10)
 OTHER INFORMATION: X = Pro-NH2
 US-09-214-371-35

Query Match 61.5%; Score 30; DB 9; Length 10;
 Best Local Similarity 62.5%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GSFFSBLW 8
 Db 2 GPTPSDLW 9

RESULT 5
 US-09-214-371-36
 Sequence 36, Application US/09214371B
 Patent No. US2001001851A1
 GENERAL INFORMATION:
 APPLICANT: Lane, David
 APPLICANT: Bottger, Volker
 APPLICANT: Pickley, Stephen
 APPLICANT: Chene, Patrick
 APPLICANT: Hochkeppel, Heinz-Kurt
 APPLICANT: Garcia-Echeverria, Carlos
 APPLICANT: Furet, Pascal
 TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
 FILE REFERENCE: 4-20937A/PCT
 CURRENT APPLICATION NUMBER: US/09/214,371B

CURRENT FILING DATE: 1999-03-26
 PRIORITY APPLICATION NUMBER: PCT/EP97/03549
 NUMBER OF SEQ ID NOS: 83
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 36
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:peptide
 NAME/KEY: VARIANT
 LOCATION: (1)
 OTHER INFORMATION: X = Ac-Cys
 NAME/KEY: VARIANT
 LOCATION: (10)
 OTHER INFORMATION: x = PRO-NH2
 US-09-214-371-36

Query Match Score 54.5%; Score 30; DB 9; Length 10;
 Best Local Similarity 62.5%; Prod. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	1 GSFFSEELW 8
Db	2 GFTFSDLW 9

RESULT 6
 US-10-221-042-1
 Sequence 1, Application US/10221042
 Publication No. US20040120946A1
 GENERAL INFORMATION:
 APPLICANT: KANEKA CORPORATION
 TITLE OF INVENTION: ADSORBENTS FOR DILATED CARDIOMYOPATHY
 FILE REFERENCE: 12218/5
 CURRENT APPLICATION NUMBER: US/10/221.042
 CURRENT FILING DATE: 2002-10-09
 PRIOR APPLICATION NUMBER: PCT/JP01/03026
 PRIOR FILING DATE: 2001-04-09
 PRIOR APPLICATION NUMBER: JP 2000-106915
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 1
 LENGTH: 13
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: peptide
 NAME/KEY: MISC FEATURE
 OTHER INFORMATION: Peptide having a binding affinity for an antibody against M2 muscarinic receptor
 OTHER INFORMATION: beta-adrenoceptor and/or an antibody against M2 muscarinic receptor
 US-10-221-042-1

Query Match Score 54.5%; Score 30; DB 16; Length 13;
 Best Local Similarity 85.7%; Prod. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1 GSFFSEEL 7
Db	7 GSFFCEL 13

RESULT 7
 US-10-155-059-13
 Sequence 13, Application US/10155059
 Publication No. US2002147173A1
 GENERAL INFORMATION:
 APPLICANT: Kaelin, William Jost, Christine

RESULT 8
 US-10-651-563-53
 Sequence 53, Application US/10651563
 Publication No. US20040072952A1
 GENERAL INFORMATION:
 APPLICANT: Sachiko MACHIDA
 APPLICANT: Ken TOKUYASU
 APPLICANT: Shigeru MATSUNAGA
 APPLICANT: Yoshiakiyo SAKAKIBARA
 APPLICANT: Masuko KOHRI
 APPLICANT: Zheseng WEN
 TITLE OF INVENTION: Novel Peptide Capable of Specifically Acting on Biological Membrar
 FILE REFERENCE: N002
 CURRENT APPLICATION NUMBER: US/10/651,563
 CURRENT FILING DATE: 2003-08-29
 PRIOR APPLICATION NUMBER: 2002-253169
 PRIOR FILING DATE: 2002-08-30
 PRIOR APPLICATION NUMBER: 2003-21198
 PRIOR FILING DATE: 2003-01-29
 NUMBER OF SEQ ID NOS: 122
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 53

LENGTH: 21
 TYPE: PCT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: synthetic peptide coded by random DNA library
 US-10-651-561-53

Query Match 54.5%; Score 30; DB 12; Length 21;
 Best Local Similarity 62.5%; Pred. No. 2.5e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GSFFSEIWN 8
 Db 3 GSFPFLNW 10

RESULT 9
 US-09-864-761-35636
 ; Sequence 35636, Application US/09864761
 ; Patent No. US20020043763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Hanzel, David R.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FILE REFERENCE: Aeonica-X-1
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 09/864,761
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/608,408
 NUMBER OF SEQ ID NOS: 49117

OTHER INFORMATION: MAP TO AC009946.1
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.2
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.8
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.96
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.9
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.1
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
 OTHER INFORMATION: EST_HUMAN HIT: AW452898.1, VALUE 5.00e-03
 US-09-864-761-35636

Query Match 54.5%; Score 30; DB 9; Length 22;
 Best Local Similarity 65.7%; Pred. No. 2.6e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FFSEIWN 8
 Db 5 YFSQNW 10

RESULT 10
 US-10-192-381-46
 ; Sequence 46, Application US/10192381
 ; Publication No. US20030170807A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
 ; APPLICANT: WORLEY, Paul
 ; APPLICANT: TU, Jian
 ; APPLICANT: XIAO, Bo
 ; APPLICANT: LEAFY, Daniel
 ; APPLICANT: BENKEN, Jutta
 ; APPLICANT: LANAHAN, Anthony
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS FILE REFERENCE: THU158-4
 CURRENT APPLICATION NUMBER: US/10/192,381
 ; CURRENT FILING DATE: 2003-07-09
 ; PRIOR APPLICATION NUMBER: US/09/377,285
 ; PRIOR FILING DATE: 1999-01-18
 ; PRIOR APPLICATION NUMBER: US 60/138,426
 ; PRIOR FILING DATE: 1999-05-10
 ; PRIOR APPLICATION NUMBER: US 60/138,493
 ; PRIOR FILING DATE: 1999-06-10
 ; PRIOR APPLICATION NUMBER: US 60/138,494
 ; PRIOR FILING DATE: 1999-05-10
 ; PRIOR APPLICATION NUMBER: US 60/097,334
 ; PRIOR FILING DATE: 1998-08-18
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 46
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-10-192-381-46

Query Match 52.7%; Score 29; DB 14; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 BLWTS 10
 Db 8 BLWTS 12

RESULT 11
 US-10-224-356-36
 ; Sequence 36, Application US/10224356
 ; Publication No. US20030144196A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company

SOFTWARE: Anymax Sequence Listing Engine vers. 1.1
 SEQ ID NO: 35636
 LENGTH: 22
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:

```

TITLE OF INVENTION: ACTIVATED T LYMPHOCYTE NUCLEIC ACID SEQUENCES AND POLYPEPTIDES EN
; TITLE OF INVENTION: SAME
; FILE REFERENCE: D0033 NP
; CURRENT APPLICATION NUMBER: US/10/224,356
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/313,957
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-224-356-16

Query Match 52.7%; Score 29; DB 14; Length 16;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 12
US-10-224-356-17
; Sequence 17, Application US/10224356
; Publication No. US2003144196A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: ACTIVATED T LYMPHOCTYE NUCLEIC ACID SEQUENCES AND POLYPEPTIDES EN
; TITLE OF INVENTION: SAME
; FILE REFERENCE: D0033 NP
; CURRENT APPLICATION NUMBER: US/10/224,356
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/313,957
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-224-356-17

Query Match 52.7%; Score 29; DB 14; Length 18;
Best Local Similarity 62.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 13
US-10-372-876-519
; Sequence 519, Application US/10372876
; Publication No. US200310204071A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: PZ021P1
; CURRENT APPLICATION NUMBER: US/10/372,876
; CURRENT FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,007
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,008
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,365
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 519
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens

```

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US-10-097-065-519
Query Match      52.7%; Score 29; DB 14; Length 21;
Best Local Similarity 44.4%; Pred. No. 3.7e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy   1 GSFFSELWT 9
     ||| :|:|
Db   13 GSVSTWTS 21

RESULT 15
US-09-186-734A-35
Sequence 35, Application US/09486734A
Patent No. US2002016732A1
GENERAL INFORMATION:
APPLICANT: Chopin, Marie-Christine
APPLICANT: Clier, Florence
APPLICANT: Erlich, S. Dusko
APPLICANT: Gautier, Michel
APPLICANT: Schouler, Catherine
APPLICANT: Institut National de la Recherche Agronomique
TITLE OF INVENTION: Resistance Mechanisms to Ic Type R/M
TITLE OF INVENTION: Bacteriophages of Lactic Acid Bacteria
FILE REFERENCE: 33339/196048
CURRENT APPLICATION NUMBER: US/09/486,734A
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: PCT/FR98/01873
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: FR 97/10885
PRIOR FILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 9
TYPE: PCR
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HsdS subunit
US-09-486-734A-35

Query Match      50.9%; Score 28; DB 9; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy   1 GSFFSEL 7
     ||| :|
Db   2 GSFFKQL 8

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Search completed: August 27, 2004, 09:48:10
Job time : 685 secs

Ig heavy chain CRD3 region (clone 3-109B) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C;Accession: PT074
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J;Exp. Med.: 173, 395-407, 1991
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A;Reference number: PT0222; MUID:1890102
 A;Accession: PT0274
 A;Molecule type: DNA
 A;Residues: 1-12 <YAM>
 A;Experimental source: B lymphocyte
 C;Keywords: heterotetramer; immunoglobulin

Query Match 45.5%; Score 25; DB 2; Length 12;
 Best Local Similarity 57.1%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 2;
 Qy 4 FSEBDWTS 10
 Db 3 YSSSWTS 9

RESULT 4

PH1602
 Ig H chain V-D-J region (wild-type clone 313) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Accession: PH1602
 R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J;Exp. Med.: 178, 117-229, 1993
 A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A;Reference number: PH1602
 A;Accession: PH1602
 A;Molecule type: DNA
 A;Residues: 1-7 <LEV>
 A;Experimental source: bone marrow pre-B lymphocyte
 C;Keywords: immunoglobulin

Query Match 43.6%; Score 24; DB 2; Length 7;
 Best Local Similarity 80.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 1;

Qy 5 SELNT 9

Db 3 SSLNT 7

RESULT 5

S60110
 hypothetical protein - human
 C;Species: Homo sapiens (man)
 C;Accession: S60110
 R;Horne, N.M.H.; Hankin, S.; Wilkinson, M.C.; Nunez, C.; Barracough, R.; McLennan, A.G.
 A;Title: Human diadenosine 5',5'--P(1),P(1)-tetraphosphate pyrophosphohydrolase is a me
 A;Reference number: S60110; MUID:96067583; PMID:7487923
 A;Accession: S60110
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-19 <THO>
 A;Cross-references: EMBL:U30313; NID:gi:1050959; PIDN: AAC50276.1; PID:gi:1050960
 Query Match 43.6%; Score 24; DB 2; Length 19;
 Best Local Similarity 50.0%; Pred. No. 4.1e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 3;

Qy 3 FSEBLNTS 10

Db 5 PYREPRRS 12

RESULT 6
 A60622
 somatostatin - spotted ratfish
 C;Species: Hydrologus colliei (spotted ratfish)
 C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 07-May-1999
 C;Accession: A60622
 R;Conlon, J.M.
 Gen. Comp. Endocrinol. 80, 314-320, 1990
 A;Title: [Ser(51)-somatosatin-14]-isolation from the pancreas of a holocephalan fish, t:
 A;Reference number: A60622; MUID:91160949; PMID:1991569
 A;Accession: A60622
 A;Molecule type: protein
 A;Residues: 1-14 <CON>
 C;Superfamily: somatostatin
 C;Keywords: hormone; neuropeptide; pancreatic islet
 F13-14/Disulfide bonds: #status experimental

Query Match 41.8%; Score 23; DB 2; Length 14;
 Best Local Similarity 55.6%; Pred. No. 4.5e+02;
 Matches 5; Conservative 2; Mismatches 2;
 Indels 0; Gaps 0;
 Qy 2 SFESSELNTS 10
 Db 5 SFFWKETTS 13

RESULT 7

A60728
 cytochrome P450 3A, troleandomycin-induced - sheep (fragment)
 C;Contains: oxidoreductase (EC 1.1.1.-.)
 N;Species: Ovis sp. (sheep)
 C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 05-Mar-1999
 C;Accession: A60728
 R;Pineau, T.; Galier, P.; Bonfils, C.; Derancourt, J.; Maurel, P.
 Biochem. Pharmacol. 39, 901-909, 1990
 A;Title: Purification of a sheep liver cytochrome P-450 from the P450IIIA gene subfamily.
 A;Reference number: A60728; MUID:90179800; PMID:2310415
 A;Accession: A60728
 A;Molecule type: protein
 A;Residues: 1-20 <PIN>
 C;Comment: This cytochrome P450 isozyme is a member of the P450IIIA family but is not fu
 C;Genetics:
 A;Gene: CYP3A
 C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
 C;Keywords: electron transfer; endoplasmic reticulum; heme; monooxygenase; oxidoreductase

Query Match 41.8%; Score 23; DB 2; Length 20;
 Best Local Similarity 57.1%; Pred. No. 6.6e+02;
 Matches 4; Conservative 0; Mismatches 3;
 Indels 0; Gaps 0;
 Qy 2 SFFSSPLW 8
 Db 6 SFSKETW 12

RESULT 8

F29501
 fibrinopeptide A - wombat
 C;Species: Vombatidae gen. sp. (wombat)
 C;Accession: F29501
 R;Blombaek, B.; Blombaek, M.; Hann, C.
 unpublished result, cited by Blombaek, B., and Blombaek, M., in Chemosystematics and Serc
 A;Reference number: A29501
 A;Accession: F29501
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-15 <PRO>
 C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 40.0%; Score 22; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 7.4e+02;
 Matches 4; Conservative 1; Mismatches 1;
 Indels 0; Gaps 0;

A;Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the context of the MHC class I molecule HLA-B7. A;Reference number: PH0135; PMID:9108843; PMID:1702137

A;Accession: PH0138
A;Molecule type: mRNA
A;Residues: 1-13 <MAB>
C;Keywords: T-cell receptor

RESULT 9

Query Match 38.2%; Score 21; DB 2; Length 13;
Best Local Similarity 37.5%; Pred. No. 9.8e+02; Indels 0; Gaps 0;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 FPFSE 6
Db 5 GSFLAE 10

A;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1638
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-les mice
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1638
A;Molecule type: DNA
A;Residues: 1-16 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 40.0%; Score 22; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
A;Accession: PH1638
R;Schmidetzky, U.; Haendler, B.; Schleuning, W.D.
submitted to the EMBL Data Library, March 1995
A;Description: Isolation and characterization of the androgen-dependent mouse cysteine-rich protein-3
A;Reference number: S53125
A;Accession: S53125
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-18 <SC3>
A;Cross-references: EMBL:X85321
R;Schmidetzky, U.; Haendler, B.; Schleuning, W.D.
Biochem. J. 309, 831-836, 1995
A;Title: Isolation and characterization of the androgen-dependent mouse cysteine-rich se
A;Reference number: S56161; MUID:93366959; PMID:7631969
A;Accession: S56161
A;Status: Preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-18 <SC2>
A;Cross-references: EMBL:X85321

Query Match 40.0%; Score 22; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SPFSE 6
Db 12 SPYSE 16

RESULT 11

Query Match 38.2%; Score 21; DB 2; Length 14;
Best Local Similarity 80.0%; Pred. No. 1.1e+03; Indels 0; Gaps 0;

Qy 5 SELWT 9
Db 2 SELWT 6

T-cell receptor beta chain V-D-J region C8 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 30-May-1997
C;Accession: PH0138
R;Martin, R.; Howell, M.D.; Jaraquemada, D.; Flerlage, M.; Richert, J.; Brostoff, S.; Lo
J. Exp. Med. 173, 19-24, 1991
A;Title: A site-specific self-cleavage reaction performed by a novel RNA in neurospora m
A;Reference number: A35105
A;Accession: A35105
A;Status: Preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Genomic code: SGCG
C;Keywords: mitochondrion

RESULT 12

Query Match 38.2%; Score 21; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 9.8e+02; Indels 0; Gaps 0;

Qy 5 SELWT 9
Db 7 ASLWT 11

Rattus sp. (rat)
C;Species: Rattus sp. (rat)
C;Accession: 151905
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 07-May-1999
R;Ma, T.; Hasewgwa, H.; Skach, W.R.; Frigeri, A.; Verkman, A.S.
Am. J. Physiol. 266, C189-C197, 1994
A;Title: Expression, functional analysis, and in situ hybridization of a cloned rat kidne
A;Reference number: 151905; PMID:7508187
A;Accession: 151905
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 1-13 <RES>
A;Cross-references: GB:S68586; NID:9545221
C;Keywords: kidney

RESULT 13

Query Match 38.2%; Score 21; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 9.8e+02; Indels 0; Gaps 0;

Qy 5 SELWT 9
Db 7 ASLWT 11

hypothetical protein - Neurospora crassa mitochondrion (fragment)
C;Species: mitochondrion Neurospora crassa
C;Accession: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 07-Dec-1999
R;Saville, B.J.; Collins, R.A.
Cell 61, 685-696, 1990
A;Title: A site-specific self-cleavage reaction performed by a novel RNA in neurospora m
A;Reference number: A35105
A;Accession: A35105
A;Status: Preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Genomic code: SGCG
C;Keywords: mitochondrion

RESULT 14

Query Match 38.2%; Score 21; DB 2; Length 14;
Best Local Similarity 80.0%; Pred. No. 1.1e+03; Indels 0; Gaps 0;

Qy 5 SELWT 9
Db 2 SELWT 6

homeotic protein Gsh-3 - mouse (fragment)

C;Species: Mus musculus (house mouse)
 C;Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 17-Oct-1997
 C;Accession: C37290; C38809
 R;Singh, G.; Kaur, S.; Stock, J.L.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Potter
 Proc. Natl. Acad. Sci. U.S.A. 88, 10706-10710, 1991
 A;Title: Identification of 10 murine homeobox genes.
 A;Reference number: A37290; MUID:92073356; PMID:1683707
 A;Accession: C37290
 A;Status: preliminary; not compared with conceptual translation.
 A;Molecule type: DNA
 A;Residues: 1-16 <SIN>
 C;Superfamily: unassigned homeobox proteins; homeobox homology
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F;1-14/Domain: homeobox homology (fragment) <HOX>
 Query Match Score 21; DB 2; Length 16;
 Best Local Similarity 42.9%; Pred. No. 1.2e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 SFPSBLW 8
 | :| :|
 Db 10 SKFKRMW 16

RESULT 15
 PH1331
 Ig heavy chain DJ region (clone C148-106) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C;Accession: PH1331
 R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shanes, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A;Title: Predominance of fetal type DTH joining in young children with B precursor lymph
 A;Reference number: PH1302; MUID:93094761; PMID:1460419
 A;Accession: PH1331
 A;Molecule type: DNA
 A;Residues: 1-17 <WAS>
 C;Keywords: heterotetramer; immunoglobulin

Query Match Score 21; DB 2; Length 17;
 Best Local Similarity 75.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 LWTS 10
 :|||
 Db 9 VWTs 12

Search completed: August 27, 2004, 09:23:33
 Job time : 40 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	21	FIBA_EQAS	16	1	P14449 equus asinus
2	20	CORZ_PRAM	11	1	P11496 periplaneta
3	20	NP3_LYNSM	13	1	P80180 lynnaea stans
4	20	SM3_MYOSC	14	1	P20750 myoxocephalus
5	20	SHS_ALLMI	14	1	P31885 alligator mississippiensis
6	20	PIL3_ECOLI	21	1	P13948 escherichia coli
7	19	FARP_MONEX	6	1	P41966 moniezia excretory
8	19	ALB2_TRAASC	15	1	P81189 trachemys scripta
9	18	LITR_PHYRO	9	1	P08946 phyllomedusa sauvagii
10	18	ARKX_LOCM1	10	1	P81626 locusta migratoria
11	18	LEFW_TIBETH	32	7	P05624 thermus thermophilus
12	18	TKNA_SYNCA	11	1	P41334 scyliorhinus stellaris
13	18	FIBA_CERSI	32	7	P14463 synurus caeruleothorax
14	18	FIBA_FELCLA	16	1	P14533 felis silvestris
15	18	FIBA_HYLCLA	32	7	P14453 hylobates macacus
16	18	FIBA_MACFU	16	1	P12893 mandrillus leucophaeus
17	18	FIBA_MANLE	32	7	P14455 mandrillus mandrillus
19	18	FIBA_ODOHE	16	1	P14459 odcoileus hemionus
20	18	FIBA_TAPTE	32	7	P14516 tapirus bairdii
21	18	FIBA_PIG	32	7	P14460 sus scrofa
22	18	FIBA_CAMDR	18	1	P14444 camelus dromedarius
23	18	FIBA_LAMGL	32	7	P14454 lama glama
24	18	TOP1_KLEAE	18	1	P46155 klebsiella pneumoniae
25	18	FIBA_BISBO	32	7	P14441 bisontis bonasus
26	18	FIBA_BOBBU	19	1	P14442 bubalus bubalis
27	18	FIBA_MUNMU	32	7	P14457 mutiacus munmu
28	18	FIBA_SHEEP	19	1	P14451 ovis aries
29	18	PQQA_SESEAE	23	1	P92aa pseudomonas aeruginosa
30	18	PQQA_PSEPK	23	1	P98av4 pseudomonas aeruginosa
31	18	PQQA_PSEST	23	1	P9Fv1 pseudomonas aeruginosa
32	17.5	LCK5_BEUMA	8	1	P19987 leucophaea
33	17	PRO3_DAGCL	23	1	P04548 periplaneta americana

ALIGNMENTS					
RESULT 1					
FIBA_EQAS					
ID	FIBA_EQAS	STANDARD;	PRT;	16 AA.	
AC	P14449;				
DT	01-JAN-1990	(Rel. 13, Created)			
DT	01-JAN-1990	(Rel. 13, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).				
GN	FGA.				
OS	Equus asinus (Donkey).				
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.				
NCBI_TaxID	9793;				
RN	[1]				
RP					
RA	Blomback B., Blomback M., Grondahl N.J.;				
RT	"Studies on fibrinopeptides from mammals."				
RL	Acta Chem. Scand. 19:1789-1791(1965).				
CC	-!- FUNCTION: Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet aggregation.				
CC	-!- SUBUNIT: Hexasmer containing 2 sets of 3 nonidentical chains (alpha, beta and gamma), linked to each other by disulfide bonds.				
CC	-!- PRIM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.				
CC	-!- KWW peptide 1, 16 AA; FIBRINOPEPTIDE A.				
FT	SEQUENCE:				
FT	Best Local Similarity 66.7%; Score 21; DB 1; Length 16;				
FT	Mismatches 0; Gaps 0; Indels 2; Pred. No. 7.7e+02;				
SQ	SEQUENCE: 16 AA; 1696 MW; 09598EB63C2A5957 CRC64;				
QY	1 GSFFSE 6				
Db	6 GEFISE 11.				
RESULT 2					
CORZ_PERAM	CORZ_PERAM	STANDARD;	PRT;	11 AA.	
ID	CORZ_PERAM				
AC	P11496;				
DT	01-OCT-1989	(Rel. 12, Created)			
DT	01-FEB-1994	(Rel. 28, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	Corazonini.				
OS	Periplaneta americana (American cockroach).				
OC	Eukaryota; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea; Blattidiae; Periplaneta.				
OC	Blattidae; Periplaneta.				
NCBI_TaxID	6378;				
RN	[1]				
RP	SEQUENCE.				

RP	SEQUENCE;	Qy	2 SFFS 5
RC	SPECIES=T. <i>scripta</i> ;	Db	18 SFFS 21
RX	MEDLINE=90341082; PubMed=1974347;		
RA	Conlon J.M., Hicks J.W.;		
RT	"Isolation and structural characterization of insulin, glucagon and somatostatin from the turtle, <i>Pseudemys scripta</i> .";		
RT	Peptides 11:461-466 (1990).		
RL	-!- FUNCTION: Somatostatin inhibits the release of somatotropin.		
CC	-!- SUBCELLULAR LOCATION: Belongs to the somatostatin family.		
CC	-!- SIMILARITY: Belongs to the somatostatin family.		
DR	PIR; C60414; C60414.		
DR	InterPro; IPR00250; Somatostatin.		
DR	PFam; PF03002; Somatostatin; 1.		
KW	Hormone.		
FT	DISULFID		
SQ	SEQUENCE 14 AA; 1640 MW; BY SIMILARITY.		
Query Match	Score 20; DB 1; Length 14;		
Best Local Similarity	36.4%; Pred. No. 1e+03;		
Matches 4;	Conservative 3; Mismatches 2; Indels 0; Gaps 0;		
Qy	2 SFFS 5 		
Db	5 NEFWKFTS 13		
RESULT 6	PIL3_ECOLI	STANDARD;	PRT; 21 AA.
AC	PIL3_ECOLI	STANDARD;	PRT; 21 AA.
DT	01-JAN-1990 (Rel. 13, Created)		
DT	01-JAN-1990 (Rel. 13, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	Fimbrial protein precursor (Pilin) (Fragment).		
GN	TRAA.		
OS	Escherichia coli.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;		
OC	Enterobacteriaceae; Escherichia.		
OX	NCBI_TaxID=562;		
RN	SEQUENCE FROM N.A.		
RP	SEQUENCE;		
RX	MEDLINE=87008371; PubMed=3531163;		
RA	Firlay B.B., Frost L.S., Parachy W.;		
RT	"Origin of transfer of IncF plasmids and nucleotide sequences of the type II oriT, traM, and traY alleles from ColB4-K98 and the type IV traY allele from R1-01-1."		
RT	J. Bacteriol. 168:132-139 (1986).		
RL	SEXPILLUS: THE PRECURSOR OF THE SEXPILLUS SUBUNIT, THE FILAMENTOUS SURFACE APPENDAGES REQUIRED FOR CELL-TO-CELL CONTACT DURING BACTERIAL CONJUGATION.		
CC	-!- SUBCELLULAR LOCATION: Secreted.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the European Bioinformatics Institute and the EMBL outstation - the Swiss Institute of Bioinformatics. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC	EMBL: M15135; AAB04666.1; .		
DR	InterPro; IPR00873; TraA.		
DR	PFam; PF0513; TraA; 1.		
KW	Plasmid; Conjugation; Fimbria.		
FT	PROBE; 1 >21		
FT	NON_TER 21 21		
SQ	SEQUENCE 21 AA; 2198 MW; 076C0D0C5E9D14EA CRC64;		
Query Match	Score 20; DB 1; Length 21;		
Best Local Similarity	100.0%; Pred. No. 1.5e+03;		
Matches 4;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
SQ	SEQUENCE 15 AA; 1733 MW; 4B7422B89FF73223 CRC64;		

Query Match 34.5%; Score 19; DB 1; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.6e+03; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 3; Standard; PRT; 9 AA.
Qy 1 GSFFSEL 7
Db 9 GHXFEXL 15

RESULT 9
LITR PHYRO STANDARD; PRT; 9 AA.
AC P08946;
ID LITR PHYRO
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Rhodei-litorin.
OS Phyllomedusa rohdei (Rohde's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8394;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=85127560; PubMed=3838283;
RA Barra D., Ersperer G.F., Simmaco M., Bossa F., Melchiorri P.,
RA Ersperer V.
RT Rohdei-litorin: a new peptide from the skin of Phyllomedusa rohdei.
RL FEBS Lett. 182:53-56 (1985).
CC 1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the bombesin/neuromedin B/ranatensin family.
CC PIR: S07241; S07241.
CC InterPro: IPR000874; Bombesin.
DR Pfam: PF02044; Bombesin; 1.
DR PROSITE: PS00057; BOMBESIN; 1.
DR Amphibian defense peptide; Bombesin family; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 9 9 AMIDATION.
SEQUENCE 9 AA; 1090 MW; 4ECCCIE861ADC377 CRC64;

Query Match 32.7%; Score 18; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
Matches 2; Conservative 2; Mismatches 2; Standard; PRT; 10 AA.
Qy 6 ELWTS 10
Db 1 QIWWAT 5

RESULT 10
AKHX LOCM1 STANDARD; PRT; 10 AA.
AC P81676;
ID AKHX LOCM1
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Peptide hormone.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridiidae; Acriidae; Oedipodinae; Locusta.
NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RA Siegert K.J.;
RL Submitted (DEC-1998) to Swiss-Prot.
CC -1- FUNCTION: Probably involved in the regulation of locust

CC intermediary metabolism, behavior and/or development.
CC -1- SUBCELLULAR LOCATION: Belongs to the AKH / HRTH / BPCH family.
CC -1- SIMILARITY: Belongs to the AKH / HRTH / BPCH family.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS000256; AKH; 1
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 1 AMIDATION.
SQ SEQUENCE 10 AA; 1222 MW; 81BFFF67AB415B9D1 CRC64;

Query Match 32.7%; Score 18; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.6e+03; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 2; Standard; PRT; 11 AA.
Qy 4 FSBLWT 9
Db 4 FSRDWWS 9

RESULT 11
LPW THETH STANDARD; PRT; 11 AA.
ID LPW THETH
AC P05624;
ID LPW THETH
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Trp operon leader peptide.
GN TRPL.
OS The genus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=89000081; PubMed=2B44259;
RA Sato S., Nakada Y., Kanaya S., Tanaka T.;
RT "Molecular cloning and nucleotide sequence of Thermus thermophilus
HB8 trpE and trpG." /
RL Biochim. Biophys. Acta 950:303-312 (1988).
CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
OF TRYPTOPHAN.

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or send an email to license@isb-sib.ch).

CC DR EMBL; X07744; CAA30565.; 1;
CC TRYptophan biosynthesis; Leader Peptide.
SQ SEQUENCE 11 AA; 1228 MW; 364B25A772DC5A7 CRC64;

Query Match 32.7%; Score 18; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.8e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 1; Standard; PRT; 11 AA.
Qy 5 SBLW 8
Db 5 SALW 8

RESULT 12
TKNA_SCYCA STANDARD; PRT; 11 AA.
ID TKNA_SCYCA
AC P41333;
ID TKNA_SCYCA
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P.
OS Scyliorhinus canicula (Spotted catshark) (Spotted catshark).

OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;	Qy	1 GSFFSE 6
OC	Elasmobranchii; Galeomorphii;	Db	5 GBFLAE 10
OC	Scyliorhinidae; Scyliorhinus.		
OX	NCBI_TAXID=1830;		
RN	[1]		
RP	SEQUENCE.		
RC	TISSUE-BRAIN;		
RX	MEDLINE=93329508; PubMed=7685693;	Qy	1 GSFFSE 6
RA	Waugh D., Wang Y., Razon N., Balment R.J., Conlon J.M.;	Db	5 GBFLAE 10
RT	"Primary structures and biological activities of substance-P-related peptides from the dogfish, <i>Scyliorhinus canicula</i> ."		
RT	Biochem. 21:4469-474 (1993).		
RL	Eur. J. Biochem. 214:469-474 (1993).		
-!-	FUNCTION: Tachykinins are active peptides which excite neurons, evoke behavioral responses, are potent vasoconstrictors and secretagogues, and contract (directly or indirectly) many smooth muscles.		
CC	-!- SIMILARITY LOCATION: Belongs to the tachykinin family.		
CC	-!- SECRETED:		
DR	PIR: S33300; S33300; DRINPRO; IPR002040; Tachy Neurokinin.		
DR	PROSITE: PS00267; TACHYKININ 1.		
KW	Tachykinin; Neuropeptide; Amidation; Neurotransmitter.		
FT	MOD-RES 11 11 AMIDATION.		
SQ	SEQUENCE 11 AA; 1278 MW; 214860DBC9D6D867 CRC64;		
Query Match	Score 32.7%; Best Local Similarity 75.0%;	Score 18; DB 1; Length 11;	
Matches	3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Pred. No. 1.8e+03;	
Qy	1 GSFF 4	CC	
Db	5 QOFF 8	CC	
RESULT 13	FIBA_SYNCA	STANDARD;	PRT; 15 AA.
ID	FIBA_SYNCA	STANDARD;	PRT; 15 AA.
AC	P14463;		
DT	01-JAN-1990 (Rel. 13, Created)		
DT	01-JAN-1990 (Rel. 13, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).		
GN	FGA.		
OS	Syncerus caffer (Cape buffalo).		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae;		
OC	Bovidae; Bovinae; Syncerus.		
NCBI_TAXID=9970;			
RN	[1]		
RP	SEQUENCE.		
RX	MEDLINE=67209145; PubMed=6033721;		
RA	Doolittle R.F., Schubert D., Schwartz S.A.; "Amino acid sequence studies on artiodactyl fibrinopeptides. I. Dromedary camel, mule deer, and cape buffalo."		
RT	Arch. Biochem. Biophys. 118:456-467(1967).		
CC	-!- FUNCTION: Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet aggregation.		
CC	-!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.		
CC	-!- PTM: Conversion of Fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.		
KW	Blood coagulation; Plasma.		
FT	PEPTIDE 1 15 FIBRINOPEPTIDE A.		
SQ	SEQUENCE 15 AA; 1480 MW; 4E998E5FOB41CC6 CRC64;		
Query Match	Score 32.7%; Best Local Similarity 50.0%;	Score 18; DB 1; Length 15;	
Matches	3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	Pred. No. 2.4e+03;	

KW Blood coagulation; plasma.
PRPTIDE 1 16 FIBRINOPEPTIDE A.
FT 16 16 C3C98EB2D6CC7D3 CRC64;
NON-TER
SQ SEQUENCE 16 AA; 1620 MN;
C3C98EB2D6CC7D3 CRC64;
Query Match 32.7%; Score 18; DB 1; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GSFFSE 6
| | :|
Db 6 GEFIAE 11

Search completed: August 27, 2004, 09:26:09
Job time : 26 secs

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OM protein - protein search, using sw model

Run on: August 27, 2004, 09:19:59 ; Search time 112 Seconds
(without alignments)
28.171 Million cell updates/sec

Title: AUDET681-1
Perfect score: 55
Sequence: 1 gsfessalwts 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 9533

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Maximum Match 100%

Listing first 45 summaries
SPTREMBL_25;*

Database :

1: sp_archeae;*
2: sp_bacteria;*
3: sp_fungi;*
4: sp_human;*
5: sp_invertebrate;*
6: sp_mammal;*
7: sp_mthc;*
8: sp_organelle;*
9: sp_phage;*
10: sp_plant;*
11: sp_rodont;*
12: sp_virus;*
13: sp_vertebrate;*
14: sp_unclassified;*
15: sp_virrus;*
16: sp_bacteriap;*
17: sp_archeap;*

Score Length DB ID Description

1 26 47.3 18 8 Q8HKI2 aponomma co

2 24 43.6 11 7 Q77895 oreochromis

3 24 43.6 11 7 Q77896 oreochromis

4 24 43.6 22 13 Q9W6D7 gallus gallus

5 24 43.6 23 6 Q9TRC6 canis familiaris

6 23 41.8 11 1 P83537 lactobacillus

7 23 41.8 13 8 Q9XL12 benisia tabacum

8 23 41.8 15 2 Q9RS56 chromatium

9 23 41.8 16 13 Q8QGA1 Q96C15 homo sapiens

10 23 41.8 20 4 Q86T45 Q93446 human herpesvirus

11 23 41.8 22 12 Q9TRT7 bos taurus

12 22 40.0 12 6 Q9TRT7 bos taurus

13 22 40.0 16 6 Q7TRB8 lilium longiflorum

14 22 40.0 17 10 Q7Y1X8 Q8hKH6 aponomma un

15 22 40.0 18 8 Q98817 oryza sativus

16 22 40.0 18 10 Q9S817

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

% Query Match Length DB ID Description

1 26 47.3 18 8 Q8HKI2 aponomma co

2 24 43.6 11 7 Q77895 oreochromis

3 24 43.6 11 7 Q77896 oreochromis

4 24 43.6 22 13 Q9W6D7 gallus gallus

5 24 43.6 23 6 Q9TRC6 canis familiaris

6 23 41.8 11 1 P83537 lactobacillus

7 23 41.8 13 8 Q9XL12 benisia tabacum

8 23 41.8 15 2 Q9RS56 chromatium

9 23 41.8 16 13 Q8QGA1 Q96C15 homo sapiens

10 23 41.8 20 4 Q86T45 Q93446 human herpesvirus

11 23 41.8 22 12 Q9TRT7 bos taurus

12 22 40.0 12 6 Q9TRT7 bos taurus

13 22 40.0 16 6 Q7TRB8 lilium longiflorum

14 22 40.0 17 10 Q7Y1X8 Q8hKH6 aponomma un

15 22 40.0 18 8 Q98817 oryza sativus

ALIGNMENTS

RESULTS

1 Q8HKI2 PRELIMINARY; PRT; 18 AA.

[1]

RN

RA

RT

RT

RL

GN

OS

OG

OC

PARASITIFORMES;

IXODIDA;

IXODIDAE;

ACARI;

OX

NCBI_TAXID=65540;

RN

RA

RT

RT

RL

GN

OS

OG

Mitochondrion.

KW

NON_TER

FT

SQ

SEQUENCE

18 AA;

2241 MW;

E50DD046AD639 CRC64;

CRC64;

Score 26;

DB 8;

Length 18;

;

Pred. No. 55.6%;

Pred. No. 5e+01;

Score 47.3%;

DB 8;

Length 18;

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Matches 4;

Mismatches 0;

Indels 0;

Gaps 0;

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OC	Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
OC	Chromatiales; Allochromatium.
RN	NCBI_TaxID=1049;
RP	SEQUENCE, AND INDUCTION.
RC	SRAIN-DSM 20451;
RX	PubMed=12112860;
RA	Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
RT	"High pressure effects stepwise altered protein expression in Lactobacillus safranensis.",
RL	Proteomics 2:765-774 (2002).
CC	-1- INDUCTION: BY ELEVATED HYDROSTATIC PRESSURE.
CC	-1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN PROTEIN IS: 65 kDa.
FT	NON_TER 1 1
FT	NON_TER 11 11
SEQENCE	11 AA; 1249 MW; D966C8231B771ADD9 CRC64;
Qy	1 GSFFFS 5 : : : 1 GSFFFA 5
Db	
RESULT 7	
ID	Q9XL12
AC	Q9XL12_1; Q9XL12_2;
DT	01-NOV-1999 (TREMBLrel. 12, Created)
DT	01-NOV-2003 (TREMBLrel. 24, Last annotation update)
DE	Cytochrome oxidase I (Fragment).
OS	Bemisia tabaci (Sweetpotato whitefly).
OG	Mitochondrion.
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aleurodidae; Aleurodidae; Aleyrodidae; Aleyrodinae; Bemisia.
OX	NCBI_TaxID=7038;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	PubMed=10583811;
RA	Frohlich D.R., Torres-Jerez I., Bedford I.D., Martham P.G., Brown J.K.;
RT	"A phylogeographical analysis of the <i>Bemisia tabaci</i> species complex based on mitochondrial DNA markers.",
RT	"Developmental expression of zebrafish HNF19, a novel hepatocyte nuclear factor-1 in zebrafish pronephros formation.";
DR	EMBL: AF11003; AA20415.1;
GO	GO:0005739; C:mitochondrion; IEA.
KW	Mitochondrion.
FT	NON_TER 1 1
SEQENCE	13 AA; 1639 MW; BDD68729F5744365 CRC64;
Qy	2 SFFSELW 8 : : : 1 SYFTSSW 7
Db	
RESULT 8	
ID	Q9RS5D6
AC	Q9RS5D6_1; Q9RS5D6_2;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE	01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DB	POLY (3-HYDROXYBUTYRIC acid) granule-associated 41 kDa protein (Fragment).
DE	Chromatium vinosum.
OS	
Qy	1 GSFFSELW 8 : : : 4 GHFFQGHW 11
Db	
RESULT 9	
ID	Q8QGA1
AC	Q8QGA1;
DT	01-JUN-2002 (TREMBLrel. 21, Created)
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE	Insulin-like growth factor-1b (Fragment).
GN	IGFB1.
OS	Brachydanio rerio (zebrafish) (Danio rerio).
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7935;	
RN	[1]
RP	SEQUENCE FROM N.A.
RX	PubMed=21261964; PubMed=11368902;
RA	Gong H.Y., Hu M.C., Chen M.H.C., Chen C.F., Weng C.F., Lin C.J.P., Lin G.H., Wu J.L.;
RA	"The characterization of prepro-insulin-like growth factor-1 Ba-2 expression and insulin-like growth factor-1 genes (devoid 81 bp) in the zebrafish (Danio rerio)."; Gene 268:67-75 (2001).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	PubMed=21261964; PubMed=11368902;
RA	Gong H.Y., Hu M.C., Chen M.H.C., Chen C.F., Weng C.F., Lin C.J.P., Lin G.H., Wu J.L.;
RA	"Developmental expression of zebrafish HNF19, a novel hepatocyte nuclear factor-1 in zebrafish pronephros formation.";
RA	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL: AF4B6298; AAL92052.1; -.
FT	NON_TER 16 16
SEQ	16 AA; 1913 MW; 1D0A5A4F917EE868 CRC64;
Qy	1 GSFFSELW 8 : : : 4 GHFFQGHW 11
Db	
RESULT 10	
ID	Q96TA5
AC	Q96TA5;
DT	01-DEC-2001 (TREMBLrel. 19, Created)
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE	MER receptor tyrosine kinase (Fragment).
DE	Homo sapiens (Human).
OS	

OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
OC	Mammalia; Butheria; Primates; Catarrhini; Hominoidea; Homo.	DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
NCBI_TaxID=9606;	[1]	DE	15 kDa amyloid protein A homolog (Fragment).
RN		OS	Bos taurus (Bovine).
RP	SEQUENCE FROM N.A. MEDLINE=20517330; PubMed=11062461;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RX	Gal A., Li Y.; Thompson D.A.; Weir J., Orth U., Jacobson S.G., Apelstedt-Sylla E.; Vollrath D.;	OC	Mammalia; Butheria; Cetartiodactyla; Ruminantia; Bovidae;
RA	RT "Mutations in MERTK, the human orthologue of the RCS rat retinal dystrophy gene, cause retinitis pigmentosa.";	OC	Bovidae; Bovinae; Bos.
RA	Nat. Genet. 26:270-271 (2000).	NCBI_TaxID=9913;	[1]
RN		RN	SEQUENCE.
RP	SEQUENCE FROM N.A. Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.	RX	Medline:92132498; PubMed:1734497;
RA	Apelstedt-Sylla E.; Vollrath D.;	RA	Veiby O.P.; Sletten K.; Husby G.; Nordstoga K.;
RA	EMBL; AF366303; ANX54121.1;	RT	"Amino acid sequence analyses of non-AA proteins from amyloid fibrils of bovine kidney".
RL	GO:0016301; F:kinase activity; IBA.	RL	Scand. J. Immunol. 35:63-65(1992).
DR	GO: GO:0004872; F:receptor activity; TEA.	FT	NON-TER 1 1
DR	Kinase; Receptor.	FT	NON-TER 12 12
FT	NON-TER 20 20	SQ	SEQUENCE 12 AA; 1503 MW; 64CDB543C6DB4AEB CRC64;
SQ	SEQUENCE 20 AA; 2232 MW; A853BEF/EECE2910 CRC64;	Query Match	Match 40.0%; Score 22; DB 6; Length 12;
Qy	1 GSFFSELW 8	Best Local Similarity	57.1%; Pred. No. 1.9e+03;
Db	11 GLFLPALW 18	Matches 4;	Mismatches 2; Indels 0; Gaps 0;
RESULT 13		Q9TR8B	PRELIMINARY;
ID	Q9TR8B	ID	PRT; 16 AA.
AC	Q9TR8B;	AC	
DT	01-MAY-2000 (TREMBLrel. 13, Created)	DT	
DE	PA28 protein (Fragment).	DE	
OS	Bos taurus (Bovine).	OS	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	
OC	Mammalia; Butheria; Cetartiodactyla; Ruminantia; Bovidae;	OC	
OX	Bovidae; Bovinae; Bos.	OX	
RN	[1] NCBI_TaxID=9913;	RN	
RP	SEQUENCE.	RX	Medline:95081084; PubMed:7989312;
RA	Mott J.D., Pramanik B.C., Moonaw C.R., Afendis S.J., Devartino G.N., Slaughter C.A.;	RA	
RA	"PA28, an activator of the 20 S proteasome, is composed of two nonidentical but homologous subunits."	RT	
RT	DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)	RT	
DT	PA28 protein (Fragment).	RL	J. Biol. Chem. 269:31466-31471(1994).
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	DR	GO: GO:0008537; C:proteasome activator complex; IEA.
DT	Human herpesvirus 1.	DR	InterPro: IPR003186; PA28_beta.
OS	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;	DR	PFam: PF02252; PA28_beta; 1.
OC	Alphaherpesvirinae; Simplexvirus.	SQ	SEQUENCE 16 AA; 1898 MW; 126D340D14EE9BDE CRC64;
OC	NCBI_TaxID=10298;	Query Match	Match 40.0%; Score 22; DB 6; Length 16;
RN		Best Local Similarity	42.9%; Pred. No. 2.5e+03;
RP	SEQUENCE FROM N.A.	Matches 3;	Mismatches 0; Indels 0; Gaps 0;
RC	STRAIN=17;	Q7Y1X8	PRELIMINARY;
RX	MEDLINE=97010565; PubMed=3020164;	ID	PRT; 17 AA.
RA	Davison B.A.J., Scott J.E./Sequence of the Major Capsid Protein Gene of Herpes Simplex virus.";	AC	
RT	DR EMBL: X04467; CAA28153.1; -	Q7Y1X8	
RT	GO: GO:0013067; P: viral assembly, maturation, egress, and rel. . . ; IEA.	DT	01-OCT-2003 (TREMBLrel. 25, Created)
DR	InterPro: IPR007629; Herpes UL20.	DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DR	Pfam: PF04544; Herpes UL20; 1.	DE	Male gametic cell-specific (fragment).
FT	NON-TER 1 1	GN	LGC1.
SQ	SEQUENCE 22 AA; 2484 MW; 2CBA43.IB3E4CLA0B CRC64;	RESULT 14	
Qy	3 FFSELWT 9	Q7Y1X8	
Db	6 FLARFWT 12	ID	
RESULT 12		Q7Y1X8	
Q9TR7		ID	
ID Q9TR7	PRELIMINARY;	AC	
AC Q9TR7	PRT; 12 AA.	Q7Y1X8	
DT 01-MAY-2000 (TREMBLrel. 13, Created)		DT	

OS *Lilium longiflorum* (Trumpet lily).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; *Lilium*.
 OX NCBI_TaxID=4690;

[1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22615576; PubMed=12729996;

RA Singh M., Bhalla P.L., Xu H., Singh M.B.;

RT "Isolation and characterization of a flowering plant male gametic
cell-specific promoter[1].";

RT FEBS Lett 542:47-52 (2003).;

RL EMBL; AY207012; AAP37155.1; -.

FT NON_TER 17 17

SQ SEQUENCE 17 AA; 1880 MW; 661B63484969679F CRC64;

Query Match 40.0%; Score 22; DB 10; Length 17;

Best Local Similarity 60.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FSEFLW 8

Db 11 FSSVW 15

RESULT 15

Q8HKH6 PRELIMINARY;

PRT: 18 AA.

ID Q8HKH6

AC Q8HKH6;

DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE NADH dehydrogenase subunit 1 (Fragment).

GN NDL.

OS *Aponomma undatum* (goanna tick).

OG Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;

OC Parasitiformes; Ixodida; Ixodidae; Aponomma.

OX NCBI_TaxID=65642;

RN SEQUENCE FROM N.A.

RA Campbell N.J.H., Murrell A., Barker S.C.;

RT "The value of idiosyncratic markers and conserved tRNA sequences from
the mitochondrial genome of hard ticks (Acari: Ixodida) for
phylogenetic inference.";

RT Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

RL EMBL; AY059193; AAL79395.1; -.

DR GO; GO:005739; C:mitochondrion; IEA.

KW Mitochondrion.

FT NON_TER 1 1

SQ SEQUENCE 18 AA; 2362 MW; 1AE724D04CC8D631 CRC64;

Query Match 40.0%; Score 22; DB 8; Length 18;

Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SFPSSEWT 9

Db 10 SFCSINFWT 17

Search completed: August 27, 2004, 09:28:10
Job time : 118 secs

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